

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 24, 2004, 20:52:22 ; Search time 3665 Seconds
(without alignments)
2498.455 Million cell updates/sec

Title: US-09-743-885A-1
Perfect score: 1353
Sequence: 1 MAGLADDSFTFGLLGNV.....NSDNALQSMKXDPRLRTSK 265

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q/cgn2.1/USPTO.spool.p/US09743865/runat_23122004.165259.9638/app_query.fasta_1.455
-DB=EST -OPMT=fasta -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09743865_@CEN_1_1_6425_@runat_23122004.165259.9638 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:.*
1: gb_est1:.*
2: gb_est2:.*
3: gb_hc:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gsa1:.*
9: gb_gsa2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	796.5	58.9	707	1	AJ558666
2	713.5	52.7	935	6	CB981330
3	706.5	52.2	747	6	CB970796
4	694	51.3	843	7	CP517565
5	691.5	51.1	771	6	CB979874
6	680.5	50.3	927	3	CNS049R7
7	677.5	50.1	765	7	CP445200
8	668.5	49.4	731	1	AJ796299
9	660.5	48.8	665	5	BU011719

10	656	48.5	872	7	CO125949	CO125949 GR_EB09L
11	656	48.5	881	7	CO123087	CO123087 GR_EB05A
12	655.5	48.4	865	7	CO125993	CO125993 GR_EB09M
13	655.5	48.4	888	7	CO121875	CO121875 GR_EB03E
14	654.5	48.4	865	7	CO121803	CO121803 GR_EB03C
15	653.5	48.3	858	7	CO090096	CO090096 GR_EA090
16	652.5	48.2	796	7	CO102085	CO102085 GR_EB002
17	652.5	48.2	796	7	CO110654	CO110654 GR_EB004
18	652.5	48.2	832	7	CO108163	CO108163 GR_EB003
19	651	48.1	737	7	CO112381	CO112381 GR_EB004
20	651	48.1	778	7	CO120905	CO120905 GR_EB024
21	650.5	48.1	1346	3	AY105872	AY105872 Zea mays
22	650	48.0	788	7	CF443959	CF443959 EST680304
23	646.5	47.8	715	7	CN125871	CN125871 RH0H1.13
24	646.5	47.8	750	4	BG840650	BG840650 MEST14-F0
25	644.5	47.6	745	4	BI422022	BI422022 EST532688
26	644	47.6	881	7	CO101149	CO101149 GR_EB002
27	640.5	47.3	737	4	BM113166	BM113166 EST560702
28	639.5	47.3	684	5	BO994945	BO994945 QGFBJ23.Y
29	635.5	47.0	786	7	CO117282	CO117282 GR_EB019
30	634	46.9	727	4	BI421916	BI421916 EST532582
31	632.5	46.7	779	7	CO099006	CO099006 GR_EA23K
32	632.5	46.7	842	7	CO087535	CO087535 GR_EA06A
33	632.5	46.7	872	7	CO094841	CO094841 GR_EA17C
34	631.5	46.7	753	7	CO099630	CO099630 GR_EA24K
35	629.5	46.5	627	6	CA137196	CA137196 SCCCR7200
36	629.5	46.5	793	5	BO118756	BO118756 EST604319
37	629	46.5	885	7	CK288429	CK288429 EST751151
38	629	46.5	942	7	CK294790	CK294790 EST751504
39	629	46.5	968	7	CK286610	CK286610 EST749332
40	628.5	46.5	847	7	CO130491	CO130491 GR_EB33E
41	627.5	46.4	1127	7	CK161576	CK161576 FGAS01414
42	623.5	46.1	774	7	CO131542	CO131542 GR_EB430
43	623.5	46.1	1101	3	CNS0A181	EX830132 Arabidops
44	623	46.0	739	2	AW441207	AW441207 EST310603
45	623	46.0	757	4	BG592948	BG592948 EST491626

ALIGNMENTS

RESULT 1
AJ558666
LOCUS
DEFINITION
AJ558666 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.1 08 c19, mRNA sequence.

ACCESSION
AJ558666
VERSION
AJ558666.1 GI:31661238
KEYWORDS
EST.
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Antirrhinum majus

REFERENCE
1 (bases 1 to 707)
Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
CONTACT: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES
Source
1. 707
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018.1 08 c19"
/tissue_type="whole plant"
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ORIGIN
Alignment Scores:

Alignment Scores:

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Percent Similarity:	83.49%	Conservative:	30
Best local Similarity:	69.72%	Mismatches:	33
Query Match:	58.87%	Indels:	3
DB:	1	Gaps:	2

US-09-743-885A-1 (1-265) X AU558666 (1-707)

Qy	4	Leuhtglaaapaspleserhellephecglyleuileuglyasnilevalserphec	23
Db	11	TTAAATGCTCAAGCCTTGCTGCTTCAATATTTGGCCATTGGGTAACATAATATCTTTCTCG	70
Qy	24	ValPheleualaaprovalProTherPheTyrrsileTyrrsarglyserSerglugly	43
Db	71	GTATTTTGGCACCAGTGCACCATTTTACAGTATTTATAGAAAGGAATCATCAGAGG	130
Qy	44	TyrglnalaleProTyrrMetValAlaleupheserlalglyleuleuleuTyrrala	63
Db	131	TTTCAGGCGAATACCGTATTCGGTGCAATCTTACGTCTCTTATCTGCTATCATATGCA	190
Qy	64	TyrrleuAaglysaenAlaleuTyrrleuValserlleaenglyphgdyCyaaAlalegu	83
Db	191	GTATTTAAGCAAGATCTTATATGATGTATATATCAATGATGATTTGGAGATATCATTTGA	250
Qy	84	LeuThyrrylleSerleupheupheThyrralaProglyserSyllePheThrgly	103
Db	251	GCAGTTTACCATCAATCTACTATATATATGATCCAAAAGTCTAAGTTTCGACGGG	310
Qy	104	TrpleuMetleuLeu--GluleuGlyAlaleuGlyMetValmetProleThyrrleu	122
Db	311	AGATTGATAGCATATTCATATGAGAGAGGTTTATAGACATGATGAGAGTGTCTTGCTTA	370
Qy	123	LeuAlaGluGlySerHiaArgValMetlleValGlyTrpIleCyaaAlaleuasnVal	142
Db	371	GCTGTTCACGGTGCAGAAAAGGTCCTCTGTGGGATGAGATGTGGCCATTATCAACGTT	430
Qy	143	AlaValPheAlaAlaProleuSerlleMetArgGlnValIleTyrrThryserValGlu	162
Db	431	GCGGTTTGGCTGCTCTTTAAGCATATGAGGCGAGTCATATAGAACCAAAAAGCGTAGG	490
Qy	163	PheMetProPheThryleuSerleupheleuThryleuCyaaAlaThMetTrpPheThyrr	182
Db	491	TTCAATGCCATTCAAGCTATCCCTTCTCTCCACCCCTTGTGGCTACAAATGAGTCTTCAAT	550
Qy	183	GlyPhePheIlySlyAspPheTyrrlleAlaPheProAenlleLeuGlyPheleuPhegly	202
Db	551	GGGTCTTCTTGTATAGGACCCCTACATCCGCTTGCCAAATGTCTTGGAATCTTATTTGGG	610
Qy	203	IleValGlnMetleuLeuTyrrPheValTyrrysAspSerlySargIleasp	220
Db	611	ATTGCTCAAAATGATTTGTATTTATCTACACAGAACGCCAA-----GACGAT	658
RESULT 2			
CB981330			
LOCUS	CB981330	935 bp	mRNA linear EST 01-MAY-2001
DEFINITION	CAB70004_11af_G09 Cabernet Sauvignon Berry Post-Veraison - CAB7		
ACCESSION	Vitis vinifera cDNA clone CAB70004_11af_G09 5', cDNA sequence.		
VERSION	CB981330		
KEYWORDS	CB981330.1 GI:30304536		
SOURCE	EST.		
ORGANISM	Vitis vinifera		
REFERENCE	Vitis vinifera		
AUTHORS	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.		
TITLE	1 (bases 1 to 935)		
JOURNAL	Goes da Silva, F., Jandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J., Jones, K. and Cook, D.		
COMMENT	Expressed sequence tags from cabernet sauvignon berries at various developmental stages		
	Unpublished (2003)		
	Contact: Douglas Cook, PhD		

CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcool@ucdavis.edu
Seq primer: ACGTACCGACATATGCC.

FEATURES

```

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB70004.T1AF_G09"
/sex="Hermaphrodite"
/dev_stage="Post-Veraison, 18-19 brix"

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ORIGIN

Alignment Scores:

Pred. No.:	1.85e-72	Length:	93
Score:	71.50	Matches:	136
Percent Similarity:	69.53%	Conservative:	56
Best local Similarity:	49.46%	Mismatches:	46
Query Match:	52.73%	Indels:	39
DB:	6	Gaps:	4

US-09-743-885A-1 (1-265) X CB981330 (1-935)

QY MetAlaGlnIleuArgAlaAspAspLeuSer-----Phe 11
 43 CTTCGCCACCTCCACGCTGAAGATGGCCTTTGTTCCCATTCACCATCTCTGGGTTTT
 QY 12 IlePheGlyLeuIleuGlyAsnIleValSerPheMetValPheIleuAlaProValProThr 31
 103 ATCTTGCGGATCTGATGTAACCTCATCTCATTCATGATGGTGAACCTTGCTCCACGCGACT 162
 Db 32 PheTyrlValIleTyrlValArgIleSerSerGluGlyTyrlGlnAlaIleProTyrlMetVal 51
 163 TTCTACCAATTTTACAAAGGAAATCCACGTAAAGGGTTTCACTGTGTTCCCTACGTGTT 222
 QY 52 AlaIeuPheSerAlaGlyLeuIleuLeuTyrlTyrlAlaTyrlLeuAlaGlyAsnAlaTyrlLeu 71
 223 GCATTATTACAGGCTATGCTTGGATATACATGCTTCTCTTAACTACGTAGTAGGCTT 282
 Db 72 IleValSerIleAsnGlyPheGlyValAsnAlaIleGluIleuThyrlTyrlIleSerLeuPheLeu 91
 283 CTGATACCATCAACTCCGTTGGCTGCTCATTTAGACACAGCTACATGTTATGTTCTT 342
 QY 92 PheTyrlAlaProArgIleSerSerIleIlePheThrGlyTrpLeuMet---LeuLeuGluLeu 110
 Db 343 GGTGTAATGCACCAAGAAAGGCTATGGAATCAACGACTGTAACCTGTTTTCTTAAGATATC 402
 QY 111 GlyAlaIleuGlyMetValMetProIleThyrlTyrlLeuAlaIleGluIleuArgIleSerHisArgVal 130
 403 TGGGATTCGGTTTCATCTGCTGTAACTCTCTCTAGCTGAAGCGGTAAACCGGTC 462
 Db 131 MetIleValaGlyTyrlIleCysAlaIleAlaIleAsnValaIleValaPheAlaAlaProLeuSer 150
 151 MetIleValaGlyTyrlIleCysAlaIleAlaIleAsnValaIleValaPheAlaAlaProLeuSer 150

Db 463 CGATTCTTGAGATGGGTTTGTCTGTTCTGCTAAGCGTTTCTTGACCCCTTTGG 522
Qy 151 ILeMeArGlnValIlelysrThlySerValGluPhMePProPherThlySerLeu 170
Db 523 ATCATAGACAAAGTATCCGAAACCAAGAGCGTTGAGTACATGCAATTTCTTATCTTT 582
Qy 171 PheLeuThlyCysAlaThrMetTrpPhePheTyGlyPhePheThlySerPheTy 190
Db 583 TTCCTCACTTGAAGTCTGTATATGCTTTTATGCTGTATGCTCAAAAGCTTTTAC 642
Qy 191 ILeAlaPheProAnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuTy 210
Db 643 ATTGCTGTCGCAAACTCCGCTGCTTCTGCTTGGGATGTTTCAATGTCCTCTACTTA 702
Qy 211 ValTyTyLeuAspSerTySarGlie---AspAspGluTySerAspProValaGlu--- 228
Db 703 ATCTACAGAAACAGAAAGAAAGTTCTGAAACGAAATTTGCTGAACTATCCGAA 762
Qy 228 ----- 228
Db 763 ATCATTGACGTTGTGAAGCTTAGACACAAATGCTGCTCAGAACTGAACCTAACCAG 822
Qy 229 -----AlaThlySerTySerTyGluGlyValGluIleIle 240
Db 823 CAGCAGCAAGATGAGACATGCGCACACAGAGAAACAAGGCTTGAATCATAGTT 879
RESULT 3
LOCUS CB970796 747 bp mRNA linear EST 30-APR-2003
DEFINITION CAB10004 Iia_F04 Cabernet Sauvignon Flower Pre-bloom - CAB1
ACCESSION CB970796
VERSION CB970796.1 GI:30253245
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosales; Vitaceae; Vitis.
1 (bases 1 to 747)
Jones da Silva,F., Iandolo,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Goes da Silva,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcocok@ucdavis.edu
Seq primer: ACCGTACCGACATATGCC.
Location/Qualifiers
1..747
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10004 Iia_F04"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom"
/lab_host="DHSAlpha"
/clone_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1:
Site_2: SfiI; CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calypters or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in

cloning as follows:
5'-AAGCAGTGGTATCAACGAGGAGGAGGATTCAGCGCGG-3' and
5'-ATTCTAGACGAGCGGCGGCGGAGGATG(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Alignment Scores:

Pred. No.:	8,95e-72	Length:	747
Score:	706.50	Matches:	133
Percent Similarity:	78.54%	Conservative:	50
Best Local Similarity:	57.08%	Mismatches:	39
Query Match:	52.22%	Indels:	11
DB:	6	Gaps:	3

US-09-743-885A-1 (1-265) x CB970796 (1-747)

Qy 1 MetAlaGlnLeuArgAlaAspAspLeuSer-----phe 11
Db 35 CTGGCCACCTCCACAGCTGAGAGATGGCTTTGCCATTACACCATCTTGTGTTT 94
Qy 12 ILePheGlyLeuLeuGlyAnIleValSerPheMetValPheLeuAlaProValProThr 31
Db 95 ATCTTGGCATCTAGAGTAACCTCATCTCATGTGTATGTTACCTGCTCAGCGACT 154
Qy 32 PheTyTyLeuIleTyTyTySarGlyTySerSerGluGlyTyTyGlnAlaIleProTyMetVal 51
Db 155 TTCCTACCAATTTACAAAGAAATCCACTGAAGGTTTCAGTCTTCCCTACGCGTT 214
Qy 52 AlaLeuPheSerAlaGlyLeuLeuLeuTyTyTyAlaTyTyLeuArgTySarAlaTyLeu 71
Db 215 GCATTATTCAGGCTATGCTTGGATATATATAGCTTCTTAACACTGATGTTACCTT 274
Qy 72 ILeValSerIleAnGlyPheGlyCysAlaIleGlnLeuThyTyTyIleSerLeuPheLeu 91
Db 275 CTCATACCATCAACTCCGTTGGCTGCGTATTGAGACCAAGCTATGTTATGTTCTT 334
Qy 92 PheTyTyAlaProArgTySerTyTyIlePheThyGlyTyTyLeuMet---LeuLeuGlnLeu 110
Db 335 GTGTATGACCGAAGAGGCTAGATCAGACTGTGAACCTGTTTTCATAGATATTC 394
Qy 111 GlnAlaLeuGlyMetValMetProIleThyTyTyLeuAlaGlnGlySerHisArgVal 130
Db 395 TGGGATTCGGTTCATCTCGCTGCTTACCTCTCTAGCTGAAGCGGTACCGGTTC 454
Qy 131 MetIleValGlyTyTyTyCysAlaAlaIleAnValAlaValPheAlaPheLeuSer 150
Db 455 CGTATCTTGAGATGGTGTGTCGTTCTGCTAAGCGTTTCTTGACCCCTTTGC 514
Qy 151 ILeMeArGlnValIlelysrThlySerValGluPhMePProPherThlySerLeu 170
Db 515 ATCATAGACAAAGTATCCGAAACCAAGAGCGTTGAGTACATGCAATTTCTTATCTTT 574
Qy 171 PheLeuThlyCysAlaThrMetTrpPhePheTyGlyPhePheThlySerPheTy 190
Db 575 TTCCTCACTTGAAGTCTGTATATGCTTTTATGCTGTATGCTCAAAAGCTTTTAC 634
Qy 191 ILeAlaPheProAnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuTy 210
Db 635 ATTGCTGTCGCAAACTCCGCTGCTTCTGCTTGGGATGTTTCAATGTCCTCTACTTA 694
Qy 211 ValTyTyLeuAspSerTySarGlie---AspAspGluTy 222
Db 695 ATCTACAAAGAAACAGAAAGAAAGTTCTGAAACGAAAG 733
RESULT 4
LOCUS CFS17565 843 bp mRNA linear EST 09-SEP-2003
DEFINITION CAP0004_IVF_A05 Vitis vinifera cv. cabernet sauvignon (Clone 8)
ACCESSION CFS17565
VERSION CFS17565.1 GI:34549333

KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
1 (bases 1 to 843)
AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J., Jones, K. and Cook, D.
TITLE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Douglas Cook, PhD
CABS Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcoc@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
FEATURES
source
1..843
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultiivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAP0004 IVF_A05"
/sex="Hermaphrodite"
/dev_stage="Onset of veraison (berry softening)"
/lab_host="DHSAlpha"
/clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Petiole - CAP"
/note="Organ: Petiole; Vector: pDNR; Site 1: SfiI; Site 2: SfiI; CAP is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 petioles. Samples were collected on July 10, 2002 from plants on the onset of veraison (berry softening). Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AGCAGTGTATTCACGACGAGTGGCCATTCAGCCGGG-3' and 5'-ATTCTAAGCGCCGAGCGCGGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Alignment Scores:

Pred. No.: 3.04e-70 Length: 843
Score: 694.00 Matches: 133
Percent Similarity: 75.30% Conservative: 53
Best Local Similarity: 53.85% Mismatches: 55
Query Match: 51.29% Indels: 6
DB: 7 Gaps: 3

US-09-743-885a-1 (1-265) x CFS17565 (1-843)

QY 9 LeuserPheillepehlyleuLeuglyAsnileValserPheMetValpHeleuAlapro 28
Db TTGGTTTATCTTCGGCATCTGAGTAACTCATCTCATTGATGCTGATCTTGTCCA 145
QY 29 ValpProthPheThylyllyleThylylserSerleuglylyTglnAlailePro 48
Db CTGCGGACTTTCACCAATTTACAAAAGAAATCCACTGAAGGGTTTCAGTCTGCC 205
QY 49 TyMetValAlaLeuPheSerAlaGlyLeuLeuLeuThyTyrAlaTyrLeuArglyAsn 68
Db TACGTGTGATTAATTCAGTGTATGCTTGGATATACCATGCTTCCCTTAACACTGAT 265
QY 69 AlaTyrleuLeuValSerleAsnGlyPheGlyCysAlailegileuLeuThyTyrIleSer 88
Db GCTAGCTTTCATCACCATCACTCGTGGCTGCTGCTGATGAGACCAAGCTACATTTGT 325

QY 89 LeuPheLeuPheThyAlaProArglySerlylePheThyGlyTyrPleuMet--Leu 107
Db ATGTTCTTGTATGATGACCGAAGGCTAGATCAGCTGGAATTCGTTTCTTA 385
QY 108 LeuGluLeuValAlaLeuGlyMetValMetProileThyTyrleuLeuAlaGlyIleSer 127
Db ATGAAATATTCGCGGATTCGGTTCATCTCTCTTAACCTCTCTTCAAGCGAGGCT 445
QY 128 HisArgValMetIleValGlyTyrPileCysAlaAlaIleAsnValAlaValPheAlaAla 147
Db AACGTCGCGATTTCTTGATGGGTTTGTCTGTGTCTCGGAACGTTTCTTGCA 505
QY 148 ProLeuSerlleMetArginValIleLysThyLysSerValGluPheMetProPheThr 167
Db CCCCTTGCATTCATGAGACAAGTTATCCGAACCAAGCCCTGGTGCATAGCCATTCTT 565
QY 168 LeuSerleuPheLeuThyLeuCysAlaThMetTyrPhePheThyGlyPhePheLys 187
Db CTATCTTTTCTTCATATGAGTCTGTATGTTGTTCTTTATGCTTGATGCTCAA 625
QY 188 AspPheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeu 207
Db GACTTTACATTCGTGTCCTCAACATCTCGGCTTGCTCTCGGATTTGTCAGATGTC 685
QY 208 LeuTyrPheValTyrLysAspSerlyArgIle--AspAspGlyLys----- 222
Db CTCTACTTAATCTACAGAAACAGAAAGTTCTGGAAAACAGAAATTCCTGAACCTA 745
QY 223 SerAspProValArgGluAlaThrLysSerlyGluGlyValGluIleIleAsnIle 242
Db TCGAACAAATCATTCGTTGAGCTTGAAGCTTAGACAAATGTGTGCTGAGATGAACTA 805
QY 243 GluAspAspAsnSerAspAsn 249
Db ACTAACCAGACGACGACAT 826
RESULT 5
CB979874
LOCUS
DEFINITION
ACCESSION
CB979874.1 GI:30303080
VERSION
CB979874.1
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
1 (bases 1 to 771)
AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J., Jones, K. and Cook, D.
TITLE Expressed sequence tags from cabernet sauvignon berries at various developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Douglas Cook, PhD
CABS Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcoc@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
FEATURES
source
1..771
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultiivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/sex="Hermaphrodite"
/dev_stage="Post-Veraison, 18-19 brix"
/lab_host="DHSAlpha"


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Qy 64 TYrLeuArgySaAnaIaTYrLeuIleValSerIleLeuGlyPheGlyCysAlaIleGlu 83
Db 214 ATCATGAGACACATGCTTATCTATCATATGATTAACACCTTGGATGTTTCATTGAA 273
Qy 84 LeuThyTYrIleSerLeuPheLeuPheTYrAlaProArgySerIlePheTYrGly 103
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Qy 104 TYrLeuMetLeuLeu---GluLeuGlyAlaLeuGlyMetValMetProIleThyTYrLeu 122
Db 334 AAGTTGATAGTACATGACATCGGTGACCTTGCTCTTAATCTTCTAGTTAACTCT 393
Qy 123 LeuAlaGlySerIleArgValMetIleValGlyTYrPheCysAlaIleAsnVal 142
Db 394 TTGGTTCCAAAACACACCGGCTCGACCGTTGGATGGGTTTGCTGCTACAGTCTC 453
Qy 143 AlaValPheAlaIleAProLeuSerIleMetArgIleValIleTYrThySerValGlu 162
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Qy 163 PheMetProPheThyLeuSerLeuPheLeuThyLeuCysAlaIleThyMetTYrPheThy 182
Db 514 TACATGCCGTTTCTTCTCTCTGCTCTGACTTAAACGCCGCTCATGTTGCTTTAT 573
Qy 183 GlyPheThySerIleAspPheTYrIleAlaPhe--ProAsnIleLeuGlyPheLeuPheG 202
Db 574 GGACTCTTATCAAGACAGATGCTATGCTATGCCCAACATTCGCTGTTTCTATTCG 633
Qy 202 IYrIleValGlnMetLeuLeuTYrPheValTYrIleAspSerIleArgIleAspArgIle 222
Db 634 GTGAGCTCATATCTATCATATCATATGATGATCAAGTTCACAGAAAACGATTTGCCAA 693
Qy 222 YSerAspProValArgGluAlaThyIleSerIleGlyValGluIleIleAsnI 242
Db 694 CAAAAACCACTCAATTAATAACGATGTTAAAGAAAGTCCGATCGTGCCTTGAAAT 753
Qy 242 IeGluAspAspAsnSerAspAsn 249
Db 754 TGCTGATGTGGATCAGACAAAT 776

RESULT 7
CF445200 765 bp mRNA linear EST 04-SEP-2003
LOCUS EST681545 normalized cDNA library of onion Allium cepa cDNA clone
DEFINITION ACAG1623, mRNA sequence.
ACCESSION CF445200
VERSION CF445200.1 GI:34467902
KEYWORDS EST.
SOURCE Allium cepa (onion)
ORGANISM Allium cepa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
Allium.
REFERENCE 1 (bases 1 to 765)
AUTHORS Hovey M.J., Cheung F., Van Aken S., Uteback T. and Town C.D.
TITLE Expressed Sequence Tags from a normalized library of mixed onion
JOURNAL classes (Allium cepa)
COMMENT Unpublished (2003)
Contact: Hovey MJ
Department of Horticulture
USDA-ARS and University of Wisconsin
1575 Linden Drive, Madison, WI 53706, USA
Tel: 608-262-1830
Fax: 608-262-4743
Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACAG1623TR. For more information:
http://havey1ab.hort.wisc.edu
Seq primer: CAG GAA ACA GCT ATG ACC.
Location/Qualifiers
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source
1. .765
/organism="Allium cepa"
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Texas Legend (roots)"
/db_xref="taxon:4679"
/clone="ACAG1623"
/tissue_type="Callus, roots, and young bulbs"
/clone_lib="normalized cDNA library of onion"
/notes="Vector: pCMVSPORT6.1-ccdb (Invitrogen); Site 1:
EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA
from callus, roots, and young bulbs were combined to
synthesize the library. Normalization to enrich for
low-copy transcripts was performed by proprietary
techniques of Invitrogen."

ORIGIN
Alignment Scores:
Pred. No.: 2,25e-68 Length: 765
Score: 677.50 Matches: 127
Percent Similarity: 77.88% Conservative: 42
Best local Similarity: 58.53% Mismatches: 47
Query Match: 50.07% Indels: 1
DB: Gaps: 1

US-09-743-885A-1 (1-265) x CF445200 (1-765)
Qy 10 SerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaProVal 29
Db 101 GCTTTCCCTTGTGCTTACTAGTATGATCTTGCTGCTCATGATGCTTCTGCTCAATT 160
Qy 30 ProThyPheTYrIleIleTYrIleArgySerSerGluIYrTYrGlnAlaIleProTYr 49
Db 161 CCAACATTTTACCGCATACCAAGAAATCAACTAGATTTAGTTCAGCTTCCTTAC 220
Qy 50 MetValAlaLeuPheSerAlaGlyLeuLeuLeuTYrTYrAlaTYrLeuArgySaAnaIa 69
Db 221 GTTGTCCTCATTTATGCTATGCTATGATATACCATTCATCAACCAAGAGAG 280
Qy 70 TYrIleIleValSerIleLeuGlyPheGlyCysAlaIleGluLeuThyTYrIleSerLeu 89
Db 281 TACCTTCTCATCATATCAACACTTTCGATGATGTTTCGTAACAAATTATCATATGATC 340
Qy 90 PheLeuPheTYrAlaProArgySerIlePheThyGlyTYrLeu---MetLeuLeu 108
Db 341 TTTCTACCTACCGCCCCCAAAAAGCAAGGTGCAACCCGAAAGATTCATCATCTCTCTA 400
Qy 109 GluLeuGlyAlaLeuGlyMetValMetProIleThyTYrLeuLeuAlaGlyIleSerHis 128
Db 401 AATGTCGGGCTAATTCCTTTAATTGTTCTATCAACTCTTCTCCCTTGCCAAAGGGGCTAGC 460
Qy 129 ArgValMetIleValGlyTYrPheCysAlaAlaIleAsnValAlaValPheAlaIlePro 148
Db 461 CGCCAAAACACTCTTGGATGGATTTGGCTGAGCTTTCAGTCACTGCTTTCGCTGACT 520
Qy 149 LeuSerIleMetArgIleValIleTYrThySerValGluPheMetProPheThyLeu 168
Db 521 TTAAAGATTAATCAGGCTAATTAATTAAGCAAAAGCGCTGATTAAGCCATTGCGGCTTG 580
Qy 169 SerLeuPheLeuThyLeuCysAlaIleThyMetTYrPheThyTYrGlyPhePheIleValAsp 188
Db 581 TCTTTTTCCTCATATGAGTGCATCATCTGTTCTCTTAATGATTTTCATCAACAAAGAC 640
Qy 189 PheTYrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeu 208
Db 641 ATCATATGAGGATTCAAAATATACGTGGATACGCTTGGAGGTTTCAGATGATCTTG 700
Qy 209 TYrPheValTYrIleAspSerIleArgIleAspAspGluIleYrSerAspPro 225
Db 701 TACATATCTCATAGATGATGAGAGCTTCTTAAGATAGCTCGAGTTACCC 751

RESULT 8
AJ796299
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LOCUS AJ796299 731 bp mRNA linear EST 11-AUG-2004
 DEFINITION AJ796299 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 018.3.10_066, mRNA sequence.
 ACCESSION AJ796299
 VERSION AJ796299.1 GI:51111627
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snapdragon)
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asteridae; lamiales; Plantaginales; Plantaginaceae; Antirrhineae;
 Antirrhinum.
 1 (bases 1 to 731)
 Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
 Antirrhinum EST collection
 Unpublished (2003)
 CONTACT: Schwarz-Sommer Z
 MOLEKULARE PFLANZENGENETIK
 MPI fuer Zuechtungsforschung
 Carl-von-Linne Weg 10, D-50829, Germany.
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 Alignment Scores:
 Pred. No.: 2 38e-67 Length: 731
 Score: 668.50 Matches: 123
 Percent Similarity: 78.97% Conservative: 46
 Best Local Similarity: 57.48% Mismatches: 43
 Query Match: 49.41% Indels: 2
 DB: 1 Gaps: 1
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 QY 6 AAlAspAspLeuSerPheIlePheGlyLeuLeuGlyAAsnIleValSerPheMetValPhe 25
 Db 86 AGTAACCAATGGCTTTCGGCTTTCGGCTTTCAGGCAACATTTGCTTCATGCTTTC 145
 QY 26 LeuAlaProVal-ProTherPheTyrllyIleTyrllyAsnGlySerSerGluGlyTyrl 45
 Db 146 CTGGACACCAAGTCCGACGCTTTATATAAATATACAGAAAGAAATCAAGTGAAGGCTTCCA 205
 QY 45 nAlaIleProTyMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlTyrlATyrl 65
 Db 206 AAGTGAACCTTAATGCTGGGCTTATTCAGTCCAGTCTGGATATACATATGATTTCT 265
 QY 65 uATGlyAsnAlaTyrlLeuIleValSerIleAsnGlyPheGlyCyAlaIleGluLeuTh 85
 Db 266 CAAAGCAGACACACCTTCTCATTAACATTAATCACTGAGATGTTTTCAAACCAT 325
 QY 85 rTyrlIleSerLeuPheLeuPheTyrlAlaProATGlySerIlePheThrlGlyTyrl 105
 Db 326 ATACATCTGCTTATCTTTTATACGCAACAAAAACACCAAGTGAACATATGAAGCT 385
 QY 105 uMet---LeuLeuGluLeuGlyAlaLeuGlyMetValMetProIleThrlTyrlLeuAl 124
 Db 386 TATTTTGTCTAAACATCTGCTGGATGGATGATGATGCTACATATTTATTTAGC 445
 QY 124 aGluGlySerIleArgValMetIleValGlyTyrlIleCyAlaAlaIleAsnValAla 144
 Db 446 CAAGAGCTCAACCGTCAACATCTGCTGGATGCTGCTGATATCTCCCTGCTGTGT 505
 QY 144 lPheAlaAlaProLeuSerIleMetArgIlnValIleTyrlThrllySerValGluPhe 164
 Db 506 ATTATATGCGCCCTTATGAGCTGAGACAAAGTTATTCGAGCTAAGAGTATAGAGTAT 565
 QY 164 tProPheThrlleuSerIleuPheThrlleuCyAlaIleThMetTrpPheThrlGlyPh 184

Db 566 GCATTTCCTTGTCTGCTTTTCTTAACCTAAGTGTGATATGATGCTTACGCGCTT 625
 QY 184 ePheIlyAspPheTyrlIleAlaPheProAsnIleLeuGlyPheLeuPheTyrlIle 204
 Db 626 ATTCGCAAGACATCAATATTCCTTAATGCTTGTGGTATCTTTGAGTGT 685
 QY 204 lGlnMetLeuLeuTyrlPheValTyrllyAspSerIlyAsnG 217
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 RESULT 9
 BU011719 665 bp mRNA linear EST 22-AUG-2002
 LOCUS OCJ16P24, mRNA sequence.
 DEFINITION OCJ16P24, mRNA sequence.
 ACCESSION BU011719
 VERSION BU011719.1 GI:22446114
 KEYWORDS EST.
 SOURCE Lactuca sativa
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asteridae; campanulide; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Lactuca.
 1 (bases 1 to 665)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
 Ellison, P., Kolhman, V., Slabaugh, M.S., Livingston, K., Zhou, Y.,
 Lai, Z., Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Composite Genome Project
 http://comgenomics.ucdavis.edu/
 Unpublished (2002)
 CONTACT: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asamundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
 belongs to config OG_CA.Config93942, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: OGJ16 row: P column: 24.
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 /note="Vector: pBRCDNA5f1AB; The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformationally made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_TISSUE=flowers pre-fertilized
 TAG_LIB=OG_EFGHJ lettuce serriola
 TAG_SEQ=CGTTGACGGG"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1 8e-66 Length: 665
 Score: 660.50 Matches: 122
 Percent Similarity: 75.35% Conservative: 40
 Best Local Similarity: 56.74% Mismatches: 52
 Query Match: 48.82% Indels: 1
 DB: 5 Gaps: 1

Qy		9	LeuserPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaPro	28
Db		17	CTTACACTGCATTTGGCCCTCTCGGCAGATGTGTGTCATTCAATCATGTGTCTTCCC	76
Oy		29	ValProThrPheTyrlsIleTyrlsArgLysSerSerGluGlyTyrlGlnAlaIlePro	48
Db		77	TTCGCCAAGCTTTTATTAAGTTTACAATAAGAAATACAGAGAGGTTTCAATCAGTGCT	136
Oy		49	TyrMetValAlaLeuPheSerAlaGlyLeuLeuTyrTyrlAlaTyrlLeuArgLysAsn	68
Db		137	TATGCGGGGGTATTATTAGCGCCATGCTTGATATATTACGATTCATTGAAGCAAT	196
Oy		69	AlaTyrlLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThryTrlleser	88
Db		197	GCGATGCTTCCTCATCACCATAACTCCGTTGGTTCCGTATTCCAAACCTTCACATTTGC	256
Oy		89	LeuPheLeuPheTyrlAlaProArgLysSerLysIlePheThr--GlyTyrlPheMetLeu	107
Db		257	TTCTTCTCTTTTAGCAACCAAGAAGGCTAGAAATCGAAAGCTTAAAGTTAATCATGTG	316
Oy		108	LeuGluLeuGlyAlaLeuGlyMetValMetProIleThrTyrlLeuAlaGluLysler	127
Db		317	ATGATAGTGTGGTGGCTTCGATGTGATGTGCTCACTACAGTTCTTGCTAATGAGACC	376
Oy		128	HisArgValMetIleValGlyTrpIleCysAlaAlaIleAsnValAlaValPheAlaAla	147
Db		377	ACTGCTGTGCAAAATAGTTGAGATGATTTGTCTCGTTCCCTTGTGTGTTTTCGTGCA	436
Oy		148	ProLeuSerIleMetArgGlnValIleLysThryLysSerValGluPheMetProPheThr	167
Db		437	CCATTGGGGGTTTGAAGCAAGTATTAAAGCAAAAACGTCGATATATGCCCCATTCCA	496
Oy		168	LeuSerLeuPheLeuThryLeuCysAlaThrMetTrpPhePheTyrlGlyPhePheLysls	187
Db		497	CTATCGGGGGCCCTCACCCCTGATGCCATGCATGTTCTTTATGCTACTTCTTCGC	556
Oy		188	AspPheTyrlIleAlaPheProAsnIleLeuGlyPheLeuPheGlyTrlIleValGlnMetLeu	207
Db		557	GACTTCAACATCGCGCATTCGCAACCTACTTGAATACAGTTTGAGTCTTCAAAATGATC	616
Oy		208	LeuTyrlPheValTyrlLysAspSerLysArgIleAspAspGluLys	222
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RESULT 10				
COL125949			872 bp mRNA linear EST 16-JUN-2004	
LOCUS			GR_EB09JL09.f GR_Eb Gossypium raimondii cDNA clone GR_EB09JL09 5'	
DEFINITION			mRNA sequence.	
VERSION			CO125949	
ACCESSION			CO125949.1 GI:48827559	
SOURCE			EST.	
ORGANISM			Gossypium raimondii	
KEYWORDS			Gossypium raimondii	
REFERENCE			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS			Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;	
			rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.	
			1 (bases 1 to 872)	
			Kim,H., Yu,Y., Kudra,D., Hatfield,J., Stum,D., Mueller,C.,	
			Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and	
			Wing,R.A.	
			Global assembly of Cotton ESTs	
TITLE			Unpublished (2004)	
JOURNAL			Contact: Rod A. Wing	
COMMENT			Arizona Genomics Institute	
			The University of Arizona	
			Forbes Building Room 303, Tucson, AZ, 85721-0036, USA	
			Tel: 520 626 9595	
			Fax: 520 621 1259	
			Email: http://genome.arizona.edu	

FEATURES	source	Location/Qualifiers
Plate: 09	row: L	column: 09.
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/lab_host="DH10B"		
/clone_1ib="GR_EB"		
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; site 2: EcoRV; library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."		
ORIGIN		
Alignment Scores:		
Prod. No.:	8. 74e-66	Length: 872
Score:	656.00	Matches: 126
Percent Similarity:	70.59%	Conservative: 54
Best Local Similarity:	49.41%	Mismatch: 61
Query Match:	48.48%	Indels: 14
DB:	7	Gaps: 3
US-09-743-885A-1 (1-265) x CO125949 (1-872)		
Qy	9	LeusePheIlePheGlyLeuLeuGlyValaniIleValSerPheMetValPheLeuAlaPro 28
Db	108	CTGGCTGTTGTTTGGTATATTAGTAACATCACTCAGCTCGTATTCTCGACCA 167
Qy	29	ValProThPheTyrlsIleTyrlsIleValSerGlySerSerGlyGlyTyrlGlnAlaIlePro 48
Db	168	GTGCCAAACATTCGTGCGATTACCAAAAAGAAATCGACTGAGCTTCCAGTCACTGCCA 227
Qy	49	TyrMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlTyrlAlaTyrlLeuArgIleValAsn 68
Db	228	TACCAAGTTCATGTTTCAGTTCGATCGCTATGCTGTTACGGCTTGATTAATAAAGGT 287
Qy	69	AlaTyrlleuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrlIleSer 88
Db	288	GCCTTCCTCTGATCACCATCAACGCTTTGGAGTGTGTGAGCATATTATATATCT 347
Qy	89	LeuPheLeuPheTyrlAlaProArgIleSerIlePheThrGlyTyrlPheMetLeu-- 107
Db	348	ATGTTCTTGCTTATGCTTCACAAAGATGACGAGATGCTGCTATGAACATTATATATCA 407
Qy	108	LeuGluLeuGlyAlaLeuGlyMetValMetProIleThrTyrlLeuAlaIleGluGlySer 127
Db	408	ATGAACCTGGGCTCTCTCTTCAATTCATCTCCACACACTTTCGCTGAAAAGCTCG 467
Qy	128	HisArgValMetIleValGlyTyrlIleCysAlaIleAlaIleAsnValAlaValPheAlaIle 147
Db	468	ATTCCGGCTCAAGTCTTGGCTGAGATTGTGTGTCGATCTCTGATCCGCTTTGGACGA 527
Qy	148	ProLeuSerIleMetArgIleValIleTyrlThrIleSerValGluPheMetProPheThr 167
Db	528	CCCTTAACATTATGCGACGAGTATTATGAAACAAAGACGCTTGAGTTGATCCCTTCACC 587
Qy	168	LeuSerLeuPheLeuThrIleuCysAlaIleMetTyrlPhePheTyrlGlyPhePheIleLys 187
Db	588	TTTATCATTTTCTCACAATGATGTCACATTAATGTTGTTATGGAATATATTAAG 647
Qy	188	AspPheTyrlIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeu 207
Db	648	GACCTCTGTAAGCTCTCCCTTAATATCTAGGCTTCATCTTGGGAGATGCTCCAGATCTT 707
Qy	208	LeuTyrlPheValTyrlsIleAspSerLysArgIleAspAspGluLysSerAspProValArg 227
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Qy	228	GluAlaThrLysSer-----LysGluGlyValGlu 237

/lab_host="DH10B"
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/note="Vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:
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Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by Agt. More glycerol clones held in -80."

ORIGIN

Alignment Scores:

Score:	9.88e-66	Length:	865
Percent Similarity:	655.50	Matches:	124
Best Local Similarity:	71.20%	Conservative:	54
Query Match:	49.60%	Mismatches:	61
	48.45%	Indels:	11
		Gaps:	2

US-09-743-885a-1 (1-265) x CO125993 (1-865)

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Db 114 CTGGCTGTTGTTTGGTATATAGTAAACATCATCTCAGCTCGTATTTCTGGACCA 173
QY 29 ValProThrPheTyrlsIleTyrlsArglySerSerGlyTyrlsAlaIlePro 48
Db 174 GTGCACACATTCCTCGATTACAAAAGAAATGAGCTGAGCTTCACGTCCAGTCCCA 233
QY 49 TyrMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlsAlaTyrlsLeuAlaAsn 68
Db 234 TACACAGTTGATGTTTCAGTGCATGCTATAGCTGATTAACGCTGATTAAGGCT 293
QY 69 AlaTyrlsLeuIleValSerIleAsnGlyPheGlyCysAlaIleGlyLeuLeuTyrlsSer 88
Db 294 GCTTCCCTTCGATCACCATCAACGCTTGGATGTGTGTGAGACTATTATATATCT 353
QY 89 LeuPheLeuPheTyrlsAlaProArglySerIlePheThrGlyTyrlsLeuLeu--- 107
Db 354 ATGTTCTTGCTTATGCTTCAAGAAATGACGAGTGCCTATGAACCTTTATATCA 413
QY 108 LeuGlyLeuGlyAlaLeuGlyMetValMetProIleThrTyrlsLeuAlaGlyIleSer 127
Db 414 ATGAACCTGGGGCTTCTCTTCATCTCATCTCCACACCTTCTGCTGAAGAGCTCG 473
QY 128 HisArgValMetIleValGlyTyrlsCysAlaIleAsnValAlaValPheAlaIle 147
Db 474 ATTCGCGTCCAAAGTCTTGGCTGATTTGCTCCATCTCTGATCCGCTTTGACACA 533
QY 148 ProLeuSerIleMetArgIleValIleTyrlsPheTyrlsSerValGlyPheMetProPheThr 167
Db 534 CCTTAACATTAATGACACGAGTTATACGAACAAAGAGCGTGAAGTTCATGCTTCCACC 593
QY 168 LeuSerPheLeuPheLeuLeuCysAlaIleThrMetTyrlsPhePheTyrlsGlyPhePheLeuLys 187
Db 594 TTATCATTTTTCCTCACATTAAGTGCAGTATGTTGCTTATGACATTTATTAAG 653
QY 188 AspPheTyrlsAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlyMetLeu 207
Db 654 GACCTCTGTGATGCTTCCCTTAATGATCTAGGCTTCACTTGGGAGATCTCCAGATGCTT 713
QY 208 LeuTyrlsPheValTyrlsAspSerLysArgIleAspArgLysSerAspProValArg 227
Db 714 CTCTACCCCATTTACACACAGTGAAGGTTAACAATAGAGAAAGAAAGACTCCAGCT 773
QY 228 GluAlaThrLysSer-----LysGlyGlyValGlu 237
Db 774 GAACAATGAAGAACATCAATGCTGCTTACCAATTAAGTGCCTCGAAGTTCACCCC 833
QY 238 IleIleIleAsnIleGlyAspAspAsnSer 247
Db 834 GTAGTTTGGATTTACACACTGATGATACA 863

RESULT 13
CO121875 COL121875 888 bp mRNA linear EST 16-JUN-2004

DEFINITION GR_Eb03E02.f GR_Eb Gossypium raimondii cDNA clone GR_Eb03E02 5',

mRNA sequence.

ACCESSION CO121875 GI:48820562

VERSION CO121875.1

KEYWORDS EST.

SOURCE Gossypium raimondii

ORGANISM Gossypium raimondii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 888)

Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,P., Mueller,C.,

Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and

Wing,R.A.

Global assembly of Cotton ESTs

Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ, 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: http://genome.arizona.edu

Plate: 03 row: E column: 02.

Location/Qualifiers

1. 888

/organism="Gossypium raimondii"

/mol_type="mRNA"

/db_xref="taxon:29730"

/clone="GR_EB03E02"

/tissue_type="floral"

/dev_stage="3 to +3 DPA"

/lab_host="DH10B"

/clone_id="GR_Eb"

/note="Vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:

ESORV; Library made by Invitrogen with RNA supplied by

Wendle lab. Directional cloned into NotI-EV. Colonies

plated/picked by Agt. More glycerol clones held in -80."

ORIGIN

Alignment Scores:

Pred. No.:	1.02e-65	Length:	888
Score:	655.50	Matches:	124
Percent Similarity:	71.20%	Conservative:	54
Best Local Similarity:	49.60%	Mismatches:	61
Query Match:	48.45%	Indels:	11
		Gaps:	2

US-09-743-885a-1 (1-265) x CO121875 (1-888)

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Db 118 CTGGCTGTTGTTTGGTATATAGTAAACATCATCTCAGCTCGTATTTCTGGACCA 177
QY 29 ValProThrPheTyrlsIleTyrlsArglySerSerGlyTyrlsAlaIlePro 48
Db 178 GTGCACACATTCCTCGATTACAAAAGAAATGACGAGATTCAGATCCAGTCCCA 237
QY 49 TyrMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlsAlaTyrlsLeuAlaAsn 68
Db 238 TACACAGTTGATGTTTCAGTGCATGCTATAGCTGATTAACGCTGATTAAGGCT 297
QY 69 AlaTyrlsLeuIleValSerIleAsnGlyPheGlyCysAlaIleGlyLeuLeuTyrlsSer 88
Db 298 GCTTCTCTTGATGATCAACACGCTTTGGATGCTGTTGATGATTAATATATCT 357
QY 89 LeuPheLeuPheTyrlsAlaProArglySerLysArgIleAspArgLysSerAspProValArg 227
Db 358 ATGTTCTTGCTATGCTTCAAGAAATGACGAGATGCGCTATGAACCTTTATATCA 417
QY 108 LeuGlyLeuGlyAlaLeuGlyMetValMetProIleThrTyrlsLeuLeuAlaGlyIleSer 127
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REFERENCE
1 (bases 1 to 858)
AUTHORS
Kam,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wang,R.A.
TITLE
Global assembly of Cotton ESTs
JOURNAL
Unpublished (2004)
COMMENT
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9395
Fax: 520 621 1259
Email: <http://genome.arizona.edu>
Plate: 09 row: O column: 05.

FEATURES
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1. 858
/organism="Gossypium raimondii"
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/clone="GR_Ea09005"
/issue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_id="GR_Ea"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; site 2:
EcoRV; library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGT. More glycerol clones held in -80."

ORIGIN

Alignment Scores:

Pred. No.: 1.67e-65 Length: 858
Score: 653.50 Matches: 124
Percent Similarity: 70.97% Conservative: 52
Best Local Similarity: 50.00% Mismatches: 61
Query Match: 48.30% Indels: 11
DB: 7 Gaps: 2

US-09-743-885A-1 (1-265) x CO090096 (1-858)

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QY 29 ValProThrPheTyrlsIleTyrlsArgIlePheSerSerGluGlyTyrlsAlaIlePro 48
Db 175 GTGCCAACATTCCTCGGATTTACAAAGAAAGATCGACTGAGAGTTCCAGTCCGCA 234
QY 49 TyMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlsAlaTyrlsLeuArgLysAsn 68
Db 235 TACCAGGTGATGTTCACTGATGCTATGCTGATTAACGCGTTCGATTAAGGGT 294
QY 69 AlaTyrlsLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrlsSer 88
Db 295 GCCTTCCTTCGATCACCATCAACGCTTTGGATGTGTTGGAGACTATTATATATCT 354
QY 89 LeuPheLeuPheTyrlsAlaProArgLysSerLysIlePheThrGlyTyrlsLeuMetLeu-- 107
Db 355 ATGTTCTTGGCTTATGCTTCAAGAAATGACGAGATGCGGCTATGAAACITTTTATATCA 414
QY 108 LeuGluLeuGlyAlaLeuGlyMetValMetProIleThrTyrlsLeuAlaGluIleSer 127
Db 415 ATGAACCTGGGGCTCTCTCTTCATCTCATCTCACACACTTTCGCTGAAAAGCTCG 474
QY 128 HisArgValMetIleValGlyTyrlsCysAlaAlaIleAsnValAlaValPheAlaAla 147
Db 475 ATTCGCGTCCAAAGTTCCTGCTGATTTGTGTCATCTCTGATACCGTCTTGGACGA 534
QY 148 ProLeuSerIleMetArgGlnValIleValThrLysSerValGluPheMetProPheThr 167
Db 535 CCTTAACATTATGACGACGAGTATACGAACAAAGAGCGTTGAGTTTCATGCTTTCACC 594

QY 168 LeuSerLeuPheLeuThrLeuCysAlaThrMetTrpPhePheTyrlsPhePheLys 187
Db 595 TTATCATTTTTCCTCACATGAGTGCAGTAAATGTTGGTTGCTTATGACTATTTATTAAG 654
QY 188 AspPheTyrlsLeaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeu 207
Db 655 GACCTCTGTAGCTCTCCCTAATGACTAGGCTTCACTTGGGAGATGCTCCAGATCCTT 714
QY 208 LeuTyrlsPheValTyrlsAspSerLysArgIleAspAspGluLysSerAspProValArg 227
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QY 228 GluAlaThrLysSer-----LysGluGlyValGlu 237
Db 775 GAACAATGAAGAACATCAATGTCGTCCTTACACATTAATGAGCTCTGAAAGTTACACCC 834
QY 238 IleIleIleAsnIleGluAspAsp 245
Db 835 GTAGTTTGGATATTCACACTGAT 858

Search completed: December 24, 2004, 23:26:17
Job time : 3873 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 24, 2004, 20:54:22 ; Search time 638 Seconds
(without alignments)
2312.807 Million cell updates/sec

Title: US-09-743-885a-1
Perfect score: 1353
Sequence: 1 MAQLRADDSFIFGLGNIV.....NSDNALQSMKXPSRLRTSK 265

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4105333 segs, 2784095677 residues
Total number of hits satisfying chosen parameters: 8210666

Minimum DB seg length: 0
Maximum DB seg length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human4.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=ext -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MXP=200000000 -USER=US09743865_QCGN_1_1912@runcat_23122004_165301_9669
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	50.3	1476	16	US-10-424-599-85620 Sequence 85620, A
2	669.5	49.5	945	18	US-10-425-115-28611 Sequence 29611, A
3	654.5	48.4	1849	16	US-10-424-599-77 Sequence 77, Appl
4	654	48.3	1102	16	US-10-425-114-32824 Sequence 32824, A
5	653.5	48.3	1500	16	US-10-425-114-15869 Sequence 15869, A
6	653.5	48.3	2436	18	US-10-425-115-28621 Sequence 28621, A
7	653	48.3	1306	16	US-10-425-114-3587 Sequence 3587, A
8	653	48.3	1415	18	US-10-425-115-28623 Sequence 28623, A
9	650.5	48.1	1703	18	US-10-425-115-29613 Sequence 29613, A
10	647.5	47.9	1513	17	US-10-767-701-14622 Sequence 14622, A
11	646.5	47.8	1141	17	US-10-437-963-15131 Sequence 15131, A
12	644.5	47.6	1487	18	US-10-739-930-5395 Sequence 5395, A
13	643	47.5	1220	16	US-10-425-114-14414 Sequence 14414, A
14	643	47.5	1360	18	US-10-425-115-28616 Sequence 28616, A
15	640	47.3	1278	16	US-10-425-114-27663 Sequence 27663, A
16	638	47.2	1306	16	US-10-424-599-66 Sequence 66, Appl
17	634	46.9	1557	17	US-10-437-963-68357 Sequence 68357, A
18	633.5	46.8	1759	17	US-10-767-701-14763 Sequence 14763, A
19	629.5	46.5	1361	16	US-10-425-114-2269 Sequence 2269, A
20	629.5	46.5	1766	18	US-10-425-115-77019 Sequence 77019, A
21	623.5	46.1	879	9	US-09-938-842A-1263 Sequence 1263, A
22	623.5	46.1	879	11	US-09-938-842A-1263 Sequence 1263, A
23	618.5	45.7	1689	16	US-10-425-114-17162 Sequence 17162, A
24	617.5	45.6	1344	16	US-10-425-114-16346 Sequence 16346, A
25	617.5	45.6	1830	18	US-10-425-115-41313 Sequence 41313, A
26	612.5	45.3	1463	16	US-10-425-114-18406 Sequence 18406, A
27	611.5	45.2	1049	17	US-10-767-795-6515 Sequence 6515, A
28	609.5	45.0	1965	16	US-10-424-599-97778 Sequence 97778, A
29	608.5	45.0	1559	16	US-10-424-599-97776 Sequence 97776, A
30	591	43.7	1404	16	US-10-424-599-133529 Sequence 133529, A
31	579.5	42.8	3076	17	US-10-437-963-48114 Sequence 48114, A
32	559.5	41.4	903	17	US-10-437-963-23863 Sequence 23863, A
33	554.5	41.0	770	17	US-10-437-963-51509 Sequence 51509, A
34	535	39.5	1103	16	US-10-424-599-117798 Sequence 117798, A
35	530.5	39.2	1276	18	US-10-425-115-128054 Sequence 128054, A
36	514	38.0	1047	16	US-10-425-115-17795 Sequence 17795, A
37	491.5	36.3	1244	18	US-10-425-115-66820 Sequence 66820, A
38	491.5	36.3	1247	16	US-10-425-114-27509 Sequence 27509, A
39	472.5	34.9	1554	16	US-10-425-114-24453 Sequence 24453, A
40	466	34.4	1195	17	US-10-437-963-5147 Sequence 5147, A
41	452.5	33.4	1183	18	US-10-739-930-2692 Sequence 2692, A
42	447	33.0	974	15	US-10-310-154-10 Sequence 10, Appl
43	441.5	32.6	1202	16	US-10-425-114-10446 Sequence 10446, A
44	429	31.7	1263	15	US-10-310-154-11 Sequence 11, Appl
45	428.5	31.7	1013	18	US-10-739-930-5185 Sequence 5185, A

ALIGNMENTS

RESULT 1
US-10-424-599-85620
; Sequence 85620, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 85620
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48329C.1

US-10-424-599-85620

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US-09-743-885A-1 (1-265) x US-10-424-599-85620 (1-1476)

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Db 276 CCACCTTTTTCACAAATCTACAGAAAAATCTACGGATGGGTTCAATCACTACCTTAT
QY 50 MetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrTyrAlaTyrLeuArgIleAsnAla 69
Db 336 ATCTGTGACATTCAGTTCAATGCTCTGATTTATTCAGCACTTGCAAAAAGATGCT 395
QY 70 ---TyrIleuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSer 88
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QY 89 LeuPheLeuPheTyrAlaProArgIleSerSerIlePheThr---GlyTyrIleMetLeu 107
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QY 108 LeuGluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluGlySer 127
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Db 636 CTTCTTTGCATCATGAACGTCATTAAGCAAGAGGTGGAAATTCATCTCTTCAGT 695
QY 168 LeuSerLeuPheLeuThrLeuCysAlaIleThrMetTyrPhePheTyrGlyPhePheIleIys 187
Db 696 TTGCTCTTCTTTGGACATTAATGCTGTATGCTGCTCTTCTTATGGCTTCTCTCAG 755
QY 188 AspPheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGluMetLeu 207
Db 756 GACTACATCAATCGCATCCCAAAATACCTTGGGTTCTTATTCGGCATATATCCAGATGGTG 815
QY 208 LeuTyrPheValTyrIleAspSerIleArgIleAspGluIleValSerAspProValArg 227
Db 816 CTGATTTTGATTTTAAAGAGCC-----AAGCCCAAGAGATTGAG 857
QY 228 GluAlaThrIleYserIleGluGlyValGluIleIleIleAsnIleGluAspAspAsn 246
Db 858 GAGCGCAACGAAGTTTCAGAACTAAATGGCATATTATTCAGCTTGGAGACCGAAT 914

RESULT 2
US-10-425-115-29611
; Sequence 29611, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21,532,221B
; CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 29611
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(945)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_127016C.1
US-10-425-115-29611
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Alignment Scores:

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Query Match:	49.48%	Indels:	7
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US-09-743-885A-1 (1-265) x US-10-425-115-29611 (1-945)

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QY 9 LeuSerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaPro 28
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QY 29 ValProThrPheTyrIleTyrIleValArgIleSerSerGluGlyTyrArgIleAlaIlePro 48
Db 292 CTGCGAGCTTCTACCGGATCTACAGAACAGATCGAGAGGGGTTTCAGTCTGCTCCG 351
QY 49 TyrMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrTyrAlaTyrLeuArgIleAsn 68
Db 352 TAGGTGTGGCCCTCTTCAAGCCATGCTGTGATCTACTACGCGCTGCTCAAGTCCAC 411
QY 69 AlaTyrLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSer 88
Db 412 GAGCTCTGCTGCTACATCAATCAATCTCCGCGGCTGCTCTCATCGAGACCTCTCATGCGCC 471
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Db 472 ATGACTCTCTCTACGCGCCCAAGAAAGAGGTGTTACGCGCAAGATCTCTCTC 531
QY 108 LeuGluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluGlySer 127
Db 532 CTCACGTGGGCGTCTCGGCTCATCTCTCTCAAGCTGCTGCTCGCGCGAG 591
QY 128 HisArgValMetIleValGlyTyrIleCysAlaAlaIleAsnValAlaValPheAlaAla 147
Db 592 CGCGCGTCTGCTCGCTCGGCTGCTGCTGCTGCTCTTCTCCGACGCTTCTGTCGCG 651
QY 148 ProLeuSerIleMetArgIleValIleIleThrIleValSerValGluPheMetProPheThr 167
Db 652 CCGCTCAGATCATCTCCGCAAGGTGAGAGCAAGAGCGTCGATTCATGACCTTCTCG 711
QY 168 LeuSerLeuPheLeuThrLeuCysAlaIleThrMetTyrPhePheTyrGlyPhePheIleIys 187
Db 712 CTCTCCCTCTCCCTCAACGTCAGCGCGCTGTCTGTCTCTCAAGCCCTCTCATCAG 771
QY 188 AspPheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGluMetLeu 207
Db 772 GACAAATACGTCCTCTGCAACGTCATCGGCTTCAAGTTCGCGCGTCCAGATGGGT 831
QY 208 LeuTyrPheValTyrIleAspSer-----IleAspGluIleAspAspGlu 221
Db 832 CTCTACGCGCTTACCGCAACGAGCGCCAGAGGTGCCATTCAAGAGAGTGGCCGAGAC 891
QY 222 IySerAsp 224
Db 892 GCGAAGAC 900
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RESULT 3

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; Sequence 77, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 77
; LENGTH: 1849
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(1849)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1006C.1
US-10-424-599-77

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Score: 654.50 Matches: 123
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Best Local Similarity: 47.67% Mismatches: 64
Query Match: 48.37% Indels: 5
DB: 16 Gaps: 4

US-09-743-885a-1 (1-265) x US-10-424-599-77 (1-1849)
QY 4 LeuArgAlaAspAspLeuSerPheIlePheGlyLeuLeuGlyValSerIleValSerPheMet 23
DB 144 ATGCATCGGAGCTTGGGCTTTGTCTTGGCGGTATGGCAACATCATCTCTTTGGA 203
QY 24 ValPheLeuAlaProValProThrPheTyrlsValIleTyrlsArgIysSerSergIugly 43
DB 204 GGTTCCTGCTGCATTCGCAACCTTTTACCAATCTACAGAAAGAAATCCACTGAAGT 263
QY 44 TyrglnAlaIleProTyrlsMetValAlaIlePheSerAlaGlyLeuLeuLeuTyrlsAla 63
DB 264 TTCCAGCTACCTCTTATGTGTGTGCACTGTTCAGTGCATGCTTGGATTCTATGCT 323
QY 64 TyrlLeu--ArgIysAsnAlaTyrlsIleValSerIleAsnGlyPheGlyCysAlaIle 82
DB 324 TTCGTAAAAGGAAAGCTGCCCTCTTCTATTAACATTGGAATTTGGATTTG 383
QY 83 GluLeuThrTyrlsSerLeuPheLeuPheTyrlsAlaProArgIysSerIysIlePheThr 102
DB 384 GAGTCATATTACCTTTCTATCTTCTTAATTAATGAGCCCAAGAAAGCAAGGCTTACAC 443
QY 103 ---GlyTrpLeuMetLeuLeuGlyAlaLeuGlyIleValMetProIleThrTyrl 121
DB 444 ATCAACCTTCTCTTCTTGAATGTGTGATTCGGGGCCATGCTTCTATCACTCTC 503
QY 122 LeuLeuAlaGlyIysSerHisArgValMetIleValGlyTyrlsCysAlaIleAsn 141
DB 504 TACCTGTCAAGGAGCAAGAGCTTTCCTATATGATGATTTGGCTTGTTCAC 563
QY 142 ValAlaValPheAlaIleProLeuSerIleMetArgIleValIleTyrlsIysSerVal 161
DB 564 ATCAGGTCTTCTGCTCACTCTTCAATTAATGAGGAGTCAATAAGAGAGAGAGCTC 623
QY 162 GluPheMetProPheThrIleuSerLeuPheLeuThrIleuCysAlaIleMetTrpPhePhe 181
DB 624 GAATACATGCATTTCTTGTTCATGCTTATTAACATCACTGCTTATAGTGTCTTC 683
QY 182 TyrgIyPhePheIysAspPheTyrlsIleAlaPheProAsnIleLeuGlyPheLeuPhe 201
```

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DB 684 TATGGCTTCTCTCAGGATTTATACGTTGCTTCCAAACCGCTGGATTGCTTC 743
QY 202 GlyIleValGlnMetLeuLeuTyrlsValTyrlsAspSerIysArgIleAspArgIu 221
DB 744 GCATTAATTCAGATGGTGTGTTGATGTACAGAAAGCCACCCCACTGACATAGAG 803
QY 222 LysSerAspProValArgGluAlaThrIysSerIysGlyValGluIleIle--Ile 240
DB 804 -----GACCACTGAGGCTCAAGATTGAATGGGCATCATCTTACCTTGTGAAGAT 857
QY 241 AsnIleGluAspAspAsnSerAspAsnAlaLeuGlnSerMetGluIysAspPhe 258
DB 858 GGAAACAATGAAACCGAATCACGGTGTGCTGTGGCAAAAGCTCATATGATTTTC 911

RESULT 4
US-10-425-114-32824
; Sequence 32824, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32824
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17025G08_FLI
US-10-425-114-32824

Alignment Scores:
Pred. No.: 4.62e-65 Length: 1102
Score: 654.00 Matches: 121
Percent Similarity: 72.93% Conservative: 46
Best Local Similarity: 52.84% Mismatches: 50
Query Match: 48.34% Indels: 12
DB: 16 Gaps: 2

US-09-743-885a-1 (1-265) x US-10-425-114-32824 (1-1102)
QY 10 SerPheIlePheGlyLeuLeuGlyValSerIleValSerPheMetValPheLeuAlaProVal 29
DB 19 GCGTTCGCTTGGCTGCTCTAGCAACGTCATCTCTTATACCTTCTGAGCCCGATA 78
QY 30 ProThrPheTyrlsIleTyrlsAspArgIysSerSergIuglyTyrglnAlaIleProTyrl 49
DB 79 CCGAGCTTTACCGCATCTTCAAGAGCAAGTGCAGCAAGAGTTTCCAGTCCCTTAC 138
QY 50 MetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlsAlaTyrlsIleuArgIysAsnAla 69
DB 139 GGGGTGGCGCTGTTCAGCGCCATGCTGTGATCTTCTACGCACTGATCAAGTCAATGAG 198
QY 70 TyrlLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrlsSerLeu 89
DB 199 ACCCTTCCTATCAATCAATCAACGCCGCCGCTGCTATTCGAAACCATCTTACATGCTCATG 258
QY 90 PheLeuPheTyrlsAlaProArgIysSerIysIlePheThrGlyTyrlsLeuMet--LeuLeu 108
DB 259 TACTTGTCTTACGCGCCCAAGAAAGCAAGCTTTCACGCGCAAGATCATGAGCCCTCTC 318
QY 109 GluLeuGlyAlaLeuGlyIleValMetProIleThrTyrlsLeuAlaGluIysSerHis 128
DB 319 AATGGGCGGCTCTTGGGGTCACTCCCTCGTCAACCTTCTCTTCAAGGATGATAG 378
```

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QY 129 ArgValMetIleValGlyTyrPheCysAlaIleAsnValAlaValPheAlaIlePro 148
|||.....|
DB 379 CGCGTTGTGCTGCTGGCTGGATCTGCGCTTCTCCGACAGTCTTGCTGGCCCA 438
QY 149 LeuSerIleMetArgGlnValIleLysThrIleSerValGluPheMetProPheThrLeu 168
|||.....|
DB 439 CTAAGCATCATGAGCGCGGTGATCCAGACGAAAGCGGTAGATGATGCTTCTCCCTC 498
QY 169 SerLeuPheLeuThrLeuCysAlaThrMetTrpPhePheTyrGlyPhePheLysAsp 188
|||.....|
DB 499 TCCCTCTCGCTCACCCCTCAGCGCGCTGCTGCTTCTCTACGCGCTCCTCATCAAGAC 558
QY 189 PheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeu 208
|||.....|
DB 559 AAATACGTTGCGCTTCCAAACGTCCTTGCTTCACTTCCGCGGTGCTCAGATGCTGCTC 618
QY 209 TyrPheValTyr-----LysAspSerLysArg 217
|||.....|
DB 619 TACGTGTTTACATGAACAGACCGCGGTGCGCTGCGTGGCGAAGATGCGCGAAG 678
QY 218 IleAspAspGlnLysSerAspProVal 226
|||
DB 679 CTTCCTCAGCTGAGACGACACGCTC 705

RESULT 5
US-10-425-114-15869
; Sequence 15869, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15869
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-096-A1_FLI
US-10-425-114-15869

Alignment Scores:
Pred. No.: 8,45e-65 Length: 1500
Score: 653.50 Matches: 122
Percent Similarity: 70.66% Conservative: 49
Best Local Similarity: 50.41% Mismatches: 54
Query Match: 48.30% Indels: 17
DB: 16 Gaps: 3

US-09-743-885A-1 (1-265) x US-10-425-114-15869 (1-1500)
QY 10 SerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaProVal 29
|||.....|
DB 263 GCGTTTCTTCCGCTTCACTAGTACGTCATCTTCATTCATGACCTTCCGCGCCGATA 322
QY 30 ProThrPheTyrLysIleTyrLysArgLysSerGlnGlyTyrGlnAlaIleProTyr 49
|||.....|
DB 323 CCGACGTTTACCGCATCTTACAGACAGTCGACGAGGCTTCCAGTCCGTTCCCTAC 382
QY 50 MetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrTyrAlaTyrLeuArgLysAsnAla 69
|||.....|
DB 383 GTGGTTGGCGCTTCAAGGCGCATGCTGATCTTTCACGACATGATCAAGTCCAAAGAG 442
QY 70 TyrLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSerLeu 89
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DB 443 ACCTTCCTCATCACCATCAACGCCCGCGGTGGTCAATCAAGACCATCAAGTGTCAAG 502
|||.....|
QY 90 PheLeuPheTyrIleAlaProArgLysSerLysIlePheThrGlyTrpLeuMet---LeuLeu 108
|||.....|
DB 503 TACTTGCTTACCGCGCCCAAGAAAGCCAGACGCTTTCACGCGCCAAAGATCATGCTCTC 562
QY 109 GluLeuGlyValLeuGlyMetValMetProIleThrTyrLeuLeuAlaGlnGlySerHis 128
|||.....|
DB 563 AATGCGCGCTTGGGGTCAATCTTCCTCACCCTTCTCCTTCAAGGATAGTAAG 622
QY 129 ArgValMetIleValGlyTyrPheCysAlaIleAsnValAlaValPheAlaIlePro 148
|||.....|
DB 623 CGGTGTGTGCTGCTGCGGTGATCTGCTGCGCTTCTCCAGTGTCTTGCGGCCA 682
QY 149 LeuSerIleMetArgGlnValIleLysThrIleSerValGluPheMetProPheThrLeu 168
|||.....|
DB 683 CTAAGCATCATGAGCGAGATCCAGACGAAAGCGGTAGATGATGCTTCTCTCCTC 742
QY 169 SerLeuPheLeuThrLeuCysAlaThrMetTrpPhePheTyrGlyPhePheLysAsp 188
|||.....|
DB 743 TCCCTCTCGCTCACCCCTCAGCGCGCTGCTGCTGCTTCTTCAAGGCTCCTCATCAAGAC 802
QY 189 PheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeu 208
|||.....|
DB 803 AAATACGTTGCGCTTCCAAACATCTGCGGTTCACCTGCGCGGTGCTCAGATGCTGCTC 862
QY 209 TyrPheValTyrLysAspSerLysArgIleAspAspGlnLysSerAspProValArgGlu 228
|||.....|
DB 863 TACGTGTTTACATGAAC-----AAGACCGCGGTGCGCGG 898
QY 229 AlaThrLysSerLysGlnGly-----ValGluIleIleIle 240
|||.....|
DB 899 ACTGCGAGGCGAAGATGCGCGCAAGCTTCTCAGCTGACAGACGACGACGCTGCTC 958
QY 241 AsnIle 242
|||
DB 959 AACATC 964

RESULT 6
US-10-425-115-29621
; Sequence 29621, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 29621
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127025C.1
US-10-425-115-29621

Alignment Scores:
Pred. No.: 1,77e-64 Length: 2436
Score: 653.50 Matches: 122
Percent Similarity: 70.66% Conservative: 49
Best Local Similarity: 50.41% Mismatches: 54
Query Match: 48.30% Indels: 17
DB: 18 Gaps: 3

US-09-743-885A-1 (1-265) x US-10-425-115-29621 (1-2436)
QY 10 SerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaProVal 29
```

Db	723	GCCTTGGCTTGGCTTACTAGTAAAGCATCTCATTTATGACCTTCTGGCCCGGATA	762
Qy	30	ProthrPheTYrLYsIleTYrLYsArgLYsSerSergLYsIleTYrGlnAlaIleProTYr	49
Db	783	CCGAGCTTCTACCGCATCTACAAAGAGCAAGTGCAGCGAAGGCTTCAGTCCGTTCCCTAC	812
Qy	50	MetValAlaIlePheSerIleAglYleuLeuTYrTYrAlaTYrIleuArgLYsAsnAla	69
Db	843	GGGTGTGCTCGTTAGCGCCATGCTGTGGATCTTCTACGACATGATCAAGTCCAAAGTCCAGAG	902
Qy	70	TYrIleuIleValSerIleAsnGlnYpheGlyCYsAlaIleGlnIleuThrTYrIleSerIleu	89
Db	903	ACCTTCTCATATCACCATCAACCCCGCGGCTGGTCATGAGACCATCTACGTCGTCATG	962
Qy	90	PheIleuPheTYrAlaProArgLYsSerIleIlePheThrGlyTYrPheIleuMet--LeuLeu	108
Db	963	TACTTTCGCTACGGCCCGCCAGAAAGCAAGCGTTTACGGCCCAAGATCATGCTCTCTC	1022
Qy	109	GlnIleuGlyAlaIleuGlyMetValIleuProIleThrTYrIleuIleuAlaGlnLYsSerHis	128
Db	1023	AATGGCGCGCTTTTGGGGTCAATCTCTCGCTCACCCCTTCTCTTCAAGGGCAGTAAG	1082
Qy	129	ArgValMetIleValGlyTYrIleCYsAlaAlaIleAsnValAlaValPheAlaAlaPro	148
Db	1083	CGCGTTGGCTGCTTGGCTGGATCTGGCGGCTTCTCGTCAGTCTTCTGTCGGCGCA	1142
Qy	149	LeuSerIleMetArgGlnValIleIleThrLYsSerValGlnIlePheMetProPheThrIleu	168
Db	1143	CTCAGCATCATGAGACGATGATCTCAGACAGAAAGCGTGGAGTCAACTGCTTCTCTC	1202
Qy	169	SerIleuPheIleuThrIleuCYsAlaIleThrMetTYrPhePheTYrGlyIlePheIleuAsp	188
Db	1203	TCCCTCTGCTCACCCCTCAGCGCCCGCTCGTGGTTCCTCTACGCGCTGCTCATCAAGGAC	1262
Qy	189	PheTYrIleAlaPheProAsnIleIleuGlyIlePheIleuPheGlyIleValGlnMetIleu	208
Db	1263	AAATACGTCGGCTTCCAAACATCTTGGGTTCACCTTGGCGGTGTCCAGATGGTGC	1322
Qy	209	TYrPheValTYrLYsAspSerLYsArgIleAspAspGlnLYsSerAspProValArgGln	228
Db	1323	TACGCTGTGTATCATAC-----AAGACGCCGCTGGCGGCG	1358
Qy	229	AlaThrLYsSerLYsGlnLYs-----ValGlnIleIleIle	240
Db	1359	ACTGCGGAGCAAGATGCGCGCAAGCTTCTCAGCTGACAGACGACGCTCTGTC	1418
Qy	241	AsnIle	242
Db	1419	AACATC	1424

RESULT 7
US-10-425-114-3587
Sequence 3587, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 3587
LENGTH: 1306
TYPE: DNA
ORGANISM: Zea mays
FEATURE:

OTHER INFORMATION: Clone ID: 700332286_FLI					
US-10-425-114-3587					
Alignment Scores:					
Pred. No.:	7,81e-65	Length:	1306		
Score:	653.00	Matches:	123		
Percent Similarity:	70.54%	Conservative:	47		
Best Local Similarity:	51.04%	Mismatches:	55		
Query Match:	48.26%	Indels:	16		
DB:	16	Gaps:	3		
US-09-743--885A-1 (1-265) x US-10-425-114-3587 (1-1306)					
QY	10	SerPheIlePhgGIyLeuGlyAnIleValSerPheMetValPheLeuAlaProVal	29		
Db	205	GGCTTGCGCCTTCGTCTCTTAAGCAACATCTTCCATGAAGACTTCGCCGCATATA	264		
QY	30	ProThrPheTyrlsIetlryrlyarlgysersergluglyrrglnalaleProTYr	49		
Db	265	CCACACCTTTACCAGCATCTACAAGAGCAAGTCGACGGAAGGTTTCCAGTCGGTTCCCTAC	322		
QY	50	MeValAlaLeuPheSeraIagIyLeuLeuLeuTYrYrAlaTYrLeuArgylasnaIa	69		
Db	325	GTGGTTGGCCTGTTCAGGCCCATGCTGTGGATCTTACGCAACGTAACTCAAGTCAAGAG	368		
QY	70	TyrIleIlleValserIleahngIyPheglIcyAlaIalegluleuthrTYrIleSerIeu	89		
Db	385	ACCTTCCTCATCACATCAACGCCGCCGCTGGCTGCATCGAAGACCATTACATCATG	444		
QY	90	PheLeuPheTYrAlaProargIyserIylePheThrgIYTPrleuMet--LeuLeu	106		
Db	445	TACCTTGCTACGGCCGCGCCAAAGAACCAAGCTGTTCAGGGCCAAGATCATGCCCCCTTC	504		
QY	109	GluleuGlYAlaleuGlYmeValmeProIethrTYrIleuLeuAlaglIySerIls	128		
Db	505	AATGGCGCGCTCTTGGGGTCATCTCTCGCTCAACCTTCTCTTCAAGGTAACTAG	564		
QY	129	ArgValmeIleValglYTPrIleCYsaIIaaleuaValaValPheAlaIaPro	148		
Db	565	CGGTTGCTGCTCTTGCTGGATCTGCGTCGCGCTTCCTCGTCAAGTCTTCTGTCGCCCA	624		
QY	149	IeuSetIleMeArGInValIleythrIySerValgluPheMeProPhThLeu	166		
Db	625	CTAAGCATATAGCGCGCTGATCCAGAAGAGCGTAGAGTCAATGCCCTTCTCCTC	684		
QY	169	SerIeuPheLeuThrlencuAlathmetTrpPheTYrGlyPhePheIyLeuAsp	188		
Db	685	TCCCTTCGCTCAACCTCAAGCGCGCTGCTGTGTTCTCTACGGCTTCCTCATAAAGAC	744		
QY	189	PheTYrIleAlaPheProAsnIleuGlYpheLeuPheglIyIleValglmetIleu	208		
Db	745	AATATAGTCGCGCTACCAAAGCTCTTGGTTTCATCTTCGCGTGGTCAAGATGTGTCTC	804		
QY	209	TyrPheValTYrIyLshapSerIyEaRglleashapglulysErAspProvalArgIlu	228		
Db	805	TACGTGTTCTACATGAAC-----AAGACCGCGGTGGCGCT	840		
QY	229	AlaThrIySerIyeglugly-----ValglullelleIleAsn	241		
Db	841	GCGGTGGGCAAGATGCGGCAAGCTTCCCTCAGCTGCAGACGACAGTCCTGTCAAC	900		
QY	242	Ile 242			
Db	901	ATT 903			
RESULT 8					
US-10-425-115-29623					
Sequence 29623 Application US/10425115					
Publication No. US20040214272A1					
GENERAL INFORMATION:					
APPLICANT: La Rosa, Thomas J.					
APPLICANT: Kovalic, David K.					
APPLICANT: Zhou, Yihua					

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 29623
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127027C.1
; US-10-425-115-29623

```

```

Alignment Scores:
Pred. No.:      8,82e-65      Length:      1415
Score:          653.00      Matches:      123
Percent Similarity: 70.54%      Conservative: 47
Best Local Similarity: 51.04%      Mismatches: 55
Query Match:    48.26%      Indels:    16
DB:             18          Gaps:         3

```

US-09-743-885a-1 (1-265) x US-10-425-115-29623 (1-1415)

```

QY      10 SerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaProVal 29
DB      262 GCGTTCCGCTTCGCGCTCTGAGCAAGTCATCTCTTCATGACCTTCGCGCCGATA 321
QY      30 ProThrPheTyrIleTyrIleValArgLysSerGluGlyTyrGlnAlaIleProTyr 49
DB      322 CCGAGCTTCAACCGCATCTCAAGAGCAAGTCGAGGAGGTTCCAGTCCGTTCCCTAC 381
QY      50 MetValAlaLeuPheSerAlaGlyLeuLeuTyrTyrAlaTyrLeuArgLysAsnAla 69
DB      382 GTGGTGGCGCTTCAAGCGCATGCTGATCTTCAACGACATCACTCAACTCAAGAG 441
QY      70 TyrLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSerIleu 89
DB      442 ACCTTCTCATCAACATCAACGCGCGCGCTGCTCATCGAGACCATCTACATCATGTCATG 501
QY      90 PheLeuPheTyrAlaProArgLysSerIlePheThrGlyTyrPleuMet---LeuLeu 108
DB      502 TACTTCGCTCAACGCGCCAGAAAGCCAGGCTGTTCACGCGCAAGATCATAGCCCTCTC 561
QY      109 GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluGlySerHis 128
DB      562 AATGGCGCGCTTGGGGTCACTCTCTGCTCAACCTTCTCTTCAAGGTAAGTAAAG 621
QY      129 ArgValMetIleValGlyTyrIleCysAlaAlaIleAsnValAlaValPheAlaAlaPro 148
DB      622 CGCGTTGGCTGCTGGCTGATCTGCGTCCGCTTCCGCAAGTGTCTTCTGCGCCCA 681
QY      149 LeuSerIleMetArgGlnValIleLysThrIleSerValGluPheMetProPheThrLeu 168
DB      682 CTAAGCATCAAGAGCGGATGATCTCAAGCGAGGAGGTAGTACATGCCCTTCTCCCTC 741
QY      169 SerLeuPheLeuThrLeuCysAlaIleThrMetTrpPheTyrGlyPhePheLysAsp 188
DB      742 TCCCTTCGCTCAACCTCAAGCGCGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
QY      189 PheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeu 208
DB      802 AATATACGCGGCTCAACCAACGCTCTGGTTCACTCTCGCGGTGTCAGATGATGTC 861
QY      209 TyrPheValTyrIleAspSerIleArgIleAspArgIleLysSerAspProValArgLys 228
DB      862 TACGTTCTCTACATGAAAC-----AAGACCGCGGTGCGGCT 897
QY      229 AlaThrLysSerLysGluGly-----ValGluIleIleLeu 241
DB      898 GCGGTGGCAAGATGCGCGCAAGCTTCTCTCACTGACGACGAGACGATCTCTGTCAAC 957

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QY      242 Ile 242
DB      958 ATT 960

```

RESULT 9

US-10-425-115-29613
Sequence 29613, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 29613

LENGTH: 1703

TYPE: DNA

ORGANISM: Zea mays

FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_127018C.1
US-10-425-115-29613

Alignment Scores:

```

Pred. No.:      2,27e-64      Length:      1703
Score:          650.50      Matches:      121
Percent Similarity: 70.25%      Conservative: 49
Best Local Similarity: 50.00%      Mismatches: 55
Query Match:    48.08%      Indels:     17
DB:             18          Gaps:         3

```

US-09-743-885a-1 (1-265) x US-10-425-115-29613 (1-1703)

```

QY      10 SerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaProVal 29
DB      525 GCGTTTCCTTCGCTCTACAGGTAACGTCATCTCTTCATGACCTTCCGCGCCGATA 584
QY      30 ProThrPheTyrIleTyrIleValArgLysSerGluGlyTyrGlnAlaIleProTyr 49
DB      585 CCGAGCTTCAACCGCATCTCAAGAGCAAGTCGAGGAGGTTCCAGTCCGTTCCCTAC 644
QY      50 MetValAlaLeuPheSerAlaGlyLeuLeuTyrTyrAlaTyrLeuArgLysAsnAla 69
DB      645 GTGGTGGCGCTTCAAGCGCATGCTGATCTTCAACGACATCACTCAACTCAAGAG 704
QY      70 TyrLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSerIleu 89
DB      705 ACCTTCTCATCAACATCAACGCGCGCGCTGCTCATCGAGACCATCTACATCATGTCATG 764
QY      90 PheLeuPheTyrAlaProArgLysSerIlePheThrGlyTyrPleuMet---LeuLeu 108
DB      765 TACTTCGCTCAACGCGCCAGAAAGCCAGGCTGTTCACGCGCAAGATCATAGCCCTCTC 824
QY      109 GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluGlySerHis 128
DB      825 AATGGCGCGCTTGGGGTCACTCTCTGCTCAACCTTCTCTTCAAGGTAAGTAAAG 884
QY      129 ArgValMetIleValGlyTyrIleCysAlaAlaIleAsnValAlaValPheAlaAlaPro 148
DB      885 CGCGTTGGCTGCTGGCTGATCTGCGTCCGCTTCCGCAAGTGTCTTCTGCGCCCA 944
QY      149 LeuSerIleMetArgGlnValIleLysThrIleSerValGluPheMetProPheThrLeu 168
DB      945 CTAAGCATCAAGAGCGGATGATCTCAAGCGAGGAGGTAGTACATGCCCTTCTCCCTC 1004
QY      169 SerLeuPheLeuThrLeuCysAlaIleThrMetTrpPheTyrGlyPhePheLysAsp 188
DB      1005 TCCCTTCGCTCAACCTCAAGCGCGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1064

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Db 380 GTGGTGGGCGTTCAGCGCATGCTGTGATCTACTACGCGCTCCAACTCCGACGAG 439
Qy 70 TyrIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSerLeu 89
Db 440 TGCCTCTCATACACATCACTCCGCTGCGCTGCTCATCGACCATTAATACATGCGCTC 499
Qy 90 PheLeuPheTyrAlaProArgLysSerLysIlePheThrGlyTyrPheMetLeuLeu-- 108
Db 500 TACCTCGCTACGCGCCCAAGAGCCCAAGATGTTTCAACCGCAAGCTCTCTCTCGCTC 559
Qy 109 GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluGlySerHis 128
Db 560 AACGTCGCGCTTCCTGCGCTATCTCTCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Qy 129 ArgValMetIleValGlyTyrPheCysAlaIleAlaIleAsnValAlaValPheAlaPro 148
Db 620 CGCATCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
Qy 149 LeuSerIleMetArgGlnValIleLysThrLysSerValGluPheMetProPheThrLeu 168
Db 680 CTTCGATCATCATCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
Qy 169 SerLeuPheLeuThrLeuCysAlaIleMetTyrPhePheTyrGlyPhePheLysLysAsp 188
Db 740 TCTCTTCTCTCTCATCATCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
Qy 189 PheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeu 208
Db 800 AAATATGTGCTCTTCCCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
Qy 209 TyrPheValTyrLysAspSerLysArgIleAspAspGluLysSerAspProValArgGlu 228
Db 860 TACCCCATGTACAGAACTCG-----ACGCCCAAG 889
Qy 229 AlaThrLysSerLysGluGlyValGlnIleIleIleAsnIleGluAspAspAsnSer 247
Db 890 GCCGTGCTGACCAAGAGGTGAGGCGGCGACGCGCACCGGCGACGACGACCACTCC 946
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RESULT 12
US-10-739-930-5395
; Sequence 5395, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739, 930
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5395
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER86_1
US-10-739-930-5395
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Alignment Scores:
Pred. No.: 9.07e-64 Length: 1487
Score: 644.50 Matches: 116
Percent Similarity: 76.11% Conservative: 56
Best Local Similarity: 51.33% Mismatch: 47
Query Match: 47.63% Indel: 7
DB: 18 Gaps: 2
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US-09-743-885a-1 (1-265) x US-10-739-930-5395 (1-1487)

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Qy 10 SerPheIlePheGlyLeuLeuGlyAsnIleValSerPheMetValPheLeuAlaProVal 29
Db 255 GCCTTGGCTTTGGCTCTTACGCAACGTATCTCTTCACTGACCTTACCTGCCCCCACTG 314
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Qy 30 ProThrPheTyrLysIleTyrLysArgLysSerSerGluGlyTyrGlnAlaIleProTyr 49
Db 315 CCGAGCTTTCACCAAACTACCGGAGCAAGTCCAGAGGGGTTCAGTGGCTCCCTTAC 374
Qy 50 MetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrTyrAlaTyrLeuArgLysAsnAla 69
Db 375 GTGGTGGGCTCTTACCGGAGATGTGTGATCTACTACCGGCTGCTCAAGTCTGACGAG 434
Qy 70 TyrIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSerLeu 89
Db 435 TGCCTCTCATACACATCACTCCGCTGCGCTGCTCATCGACCATTAATACATGCGCTC 494
Qy 90 PheLeuPheTyrAlaProArgLysSerLysIlePheThrGly--TyrPheMetLeuLeu 108
Db 495 TACCTCACCTATGACCAAGAGCCCAAGCTCTTCAACCGCAAGATCTCTCTCTCTCTCT 554
Qy 109 GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluGlySerHis 128
Db 555 AATGTGGGTGTGCTTCTTATCTCTCTCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCT 614
Qy 129 ArgValMetIleValGlyTyrPheCysAlaIleAlaIleAsnValAlaValPheAlaPro 148
Db 615 CGGCTGCTATGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
Qy 149 LeuSerIleMetArgGlnValIleLysThrLysSerValGluPheMetProPheThrLeu 168
Db 675 CTCAGCTCATATCCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 734
Qy 169 SerLeuPheLeuThrLeuCysAlaIleMetTyrPhePheTyrGlyPhePheLysLysAsp 188
Db 735 TCTCTTCTCTCTCATCATCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 794
Qy 189 PheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeu 208
Db 795 AAATATGTGCTCTTCCCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 854
Qy 209 TyrPheValTyrLysAspSer-----LysArgIleAspAspGluLys 222
Db 855 TACGCCCTCTACCGCAACGCGCATGCTTCAACCGGCTTCCCAAGAGGTGAGTGTGAT 914
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RESULT 13
US-10-425-114-14414
; Sequence 14414, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14414
; LENGTH: 1220
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB189-020-A7_FLI
US-10-425-114-14414
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Alignment Scores:
Pred. No.: 9.97e-64 Length: 1220
Score: 643.00 Matches: 120
Percent Similarity: 70.71% Conservative: 49
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Best Local Similarity:	50.21%	Mismatches:	58
Query Match:	47.52%	Indels:	12
DB:	16	Gaps:	3

US-09-743-885A-1 (1-265) X US-10-425-114-14414 (1-1220)

[illegible]

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127020C.1
US-10-425-115-29616

Alignment Scores:

US-09-743-885A-1 (1-265) X US-10-425-115-29616 (1-1360)

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OY      10 SerPheIlePheGlyLeuLeuGlyValLeuIleValSerPheMetValPheLeuAlaProVal 29
      11 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      230 GCATTCACTTCGGGCTCCCTAGGCAAGCGATCTCTTCATGACCTTCCTGGGCCCCGATA 289

OY      30 ProThrPheTyrlsAlleTyrlsArglySerSerGluGlyTyrlGlnAlaIleProTy 49
      31 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      290 CCGAGCTTCACTCCGCGATCTTACAAAGGACAAGTGCAGCGAGGGCTTCCAGTCCGCTGAC 349

OY      50 MetValAlaLeuPheSerAlaGlyLeuLeuLeuTyrlTyrlAlaTyrlLeuArglyAsnAla 69
      51 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      350 GTGGTGGCCCTGTTAGGCGCCATGCTGTGGATCTTCTTACGCGCTGATCAAGTCCAAAGAC 409

OY      70 TyrlLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrlIleSerLeu 89
      71 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      410 ACGTTCCTCATCAACCATCAACGCGCGCGCTCGATGAGAACCGCTTACGCGTCAATG 469

OY      90 PheLeuPheTyrlAlaProArglySerIleIlePheThylTyrlLeuMet---LeuLeu 108
      91 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      470 TACTTCGTTCAGCCACCAAGAGGGCAGGATGTTACCGCCAAATCAATGCTCTTCCTC 529

OY      109 GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrlLeuLeuAlaGluGlySerHis 128
      110 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      530 AAGCTCGGCGGCTTCGGGGTCCATCTCCTCCCTCAACCTTCTCTCTTCAAGGTGACAAAG 589

OY      129 ArgValMetIleValGlyTyrlPheCysAlaAlaIleAsnValAlaValPheAlaIlePro 148
      130 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      590 CGCGTCGTCATGCTTGGCTGTGATCTCGCGCTTCTCCTGACGCTCTTCTCGCGGCCG 649

OY      149 LeuSerIleMetArgGlnValIleLeuThrIlySerValIleGluPheMetProPheThrLeu 168
      150 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      650 CTCAGCATCAAGAGCGGGGTGATCCAGACCAAGACGCTGAGTACATGCCCTTCTCCCTC 709

OY      169 SerIleuPheLeuThrLeuCysAlaIleThrMetTyrlPhePheTyrlGlyPhePheIlyAsp 188
      170 TCCCTCTCGCTCAACCTCCTCAGCGCGCTCGCTCGTTCCTTCAAGGCTCTCATCAAGGAC 769

OY      189 PheTyrlIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValIleMetLeuLeu 208
      190 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      770 AAATACGTCGCGCTTCCAAACATCTTGGCTTACCTTCGGGTGTGTCAGATGGTGC 829

OY      209 TyrlPheValTyrlsAspSerIlyArgIleAspArgGluIlySerAspProValArgGlu 228
      210 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      830 TACGTGCGTGTACATGAACAAGACGCGCGCTC-----CGGTGTCGAC 871

OY      229 Ala-----ThrIlySerIlyGluGlyValGluIleIleIleAsnIle 242
      230 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      872 GGCAAGGCTGCGGCAAGCTTCCCTCAGCTGCAGATGACACAGTGTCTGTCAACGTC 928

RESULT 15
US-10-425-114-27663
; Sequence 27663, Apolication US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 24, 2004, 20:51:27 ; Search time 103 Seconds
(without alignments)
1828.729 Million cell updates/sec

Title: US-09-743-885a-1
Perfect score: 1353
Sequence: 1 MAQLRADDSIFGLGNIV.....NSDNALQSMKDPFRRTSK 265

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 35339441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -NOR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=ptc -NOR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15
-USER=US09743885.QCEN_1_128.runal_23122004_165259_9650 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/prodata/1/ina/backfill1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	206.5	15.3	272	US-09-313-294A-448	Sequence 448, App
2	195.5	14.4	1314	US-09-589-360B-54	Sequence 54, Appl
3	107.5	7.9	2160	US-08-902-853-4	Sequence 4, Appl
4	107	7.9	759	US-09-248-796A-12834	Sequence 12834, A
5	103.5	7.6	503	US-09-270-767-8810	Sequence 8810, Ap
6	103.5	7.6	503	US-09-270-767-24092	Sequence 24092, A
7	103	7.6	640681	US-09-790-989-1	Sequence 1, Appl
8	101.5	7.5	1188	US-09-134-000C-2036	Sequence 2036, Ap
9	101	7.5	1280	US-09-199-737-1	Sequence 1, Appl
10	101	7.5	1280	US-08-900-230-1	Sequence 1, Appl
11	101	7.5	1280	US-09-058-333A-1	Sequence 1, Appl
12	100.5	7.4	1389	US-09-328-352-1371	Sequence 1371, Ap

13	99	7.3	864	US-09-543-681A-1110	Sequence 1110, Ap
14	99	7.3	1146	US-09-134-001C-1135	Sequence 1135, Ap
15	98.5	7.3	1704	US-09-711-164-238	Sequence 238, App
16	98	7.2	885	US-09-328-352-3427	Sequence 3427, Ap
17	98	7.2	978	US-09-328-352-1634	Sequence 1634, Ap
18	97.5	7.2	1449	US-09-328-352-3658	Sequence 3658, Ap
19	97	7.2	699	US-09-543-681A-686	Sequence 686, App
20	97	7.2	1323	US-09-248-796A-6305	Sequence 6305, Ap
21	97	7.2	1664976	US-08-916-421B-1	Sequence 1, Appl
22	97	7.2	1664976	US-08-692-570-1	Sequence 1, Appl
23	96.5	7.1	13856	US-08-956-171B-31	Sequence 31, Appl
24	96.5	7.1	13856	US-08-781-986A-31	Sequence 31, Appl
25	96	7.1	2395	US-09-270-767-11401	Sequence 11401, A
26	95.5	7.1	297	US-09-313-294A-7017	Sequence 7017, Ap
27	95.5	7.1	342	US-08-961-527-206	Sequence 206, App
28	95.5	7.1	1830121	US-09-557-884-1	Sequence 1, Appl
29	95.5	7.1	1830121	US-09-643-990A-1	Sequence 1, Appl
30	95.5	7.1	1830121	US-10-329-960-1	Sequence 1, Appl
31	95	7.0	1230025	US-09-198-452A-1	Sequence 1, Appl
32	93.5	6.9	1058	US-09-016-434-1206	Sequence 1206, Ap
33	93.5	6.9	1296	US-09-489-039A-1107	Sequence 1107, Ap
34	93.5	6.9	1536	US-09-252-991A-11740	Sequence 11740, A
35	93.5	6.9	1536	US-09-489-039A-1037	Sequence 1037, Ap
36	93.5	6.9	1537	US-09-252-991A-15015	Sequence 15015, A
37	92.5	6.8	1310	US-09-944-807-1	Sequence 1, Appl
38	92.5	6.8	2163	US-09-134-000C-2226	Sequence 2226, Ap
39	92.5	6.8	2631	US-09-023-655-1083	Sequence 1083, Ap
40	92.5	6.8	1664976	US-08-916-421B-1	Sequence 1, Appl
41	92.5	6.8	1664976	US-09-692-570-1	Sequence 1, Appl
42	92	6.8	1977	US-09-614-891-5	Sequence 5, Appl
43	91.5	6.8	1014	US-10-061-943A-3	Sequence 3, Appl
44	91.5	6.8	1140	US-09-016-434-750	Sequence 750, App
45	91.5	6.8	1301	US-08-467-948A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-313-294A-448
; Sequence 448, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ialugdi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 448
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549251H1
; US-09-313-294A-448

Alignment Scores:

Pred. No.: 4.5e-17
Score: 206.50
Percent Similarity: 73.26%
Best Local Similarity: 51.16%
Query Match: 15.26%
DB: 4
Gaps: 1

US-09-743-885A-1 (1-265) x US-09-313-294A-448 (1-272)

QY 80 CysAlIISGLuLeuThrTyrIleSerLeuPheLeuPheTyrNlaProArglySerLyg 99
Db 15 TGGCATCGAGACCATCTACATCGTCATGTACTTGGTCACGCGCCCAAGAACGCAAG 74


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TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HNT2NOT01
; CLONE: 493014
; US-08-902-853-4

Alignment Scores:
Pred. No.: 0.00279 Length: 2160
Score: 107.50 Matches: 71
Percent Similarity: 38.78% Conservative: 31
Best Local Similarity: 27.00% Mismatches: 97
Query Match: 7.95% Indels: 65
DB: Gaps: 14

US-09-743-885a-1 (1-265) x US-08-902-853-4 (1-2160)
QY 1 MetAlaGlnLeuArgAlaAspSerPheIlePheGlyLeuGlyAsnIleVal 20
DB 494 CTCAGAAGATTCGAGAGAGCGAGCTGAGATTCACATTTTACTGATTGCC--TTCAAT 550
QY 21 SerPheMetValPheLeuAlaProValProThrPheTyrIleTyrIleTyrIleTyrSer 40
DB 551 GCCGCGATGCGCGCTGATGTGATTAACCTGCTGTTATGACATG--AAGAAAGTT 604
QY 41 SerGlnGlyTyr-----GlnAlaIlePro-----TyrMetValAla 52
DB 605 TGGAGAGGATATCCCTACAGAGCACTATCCCTCCAGATTGTTGACTACATGATGAA 664
QY 53 LeuPhe-SerAlaGlyLeuLeuTyrTyrAlaTyrLeuArgLysAsnAlaTyrLeuI 72
DB 665 CTTTCCTTCTACTGCT----- 680
QY 72 eValSerIleAsnGlyPheGlyCysAlaIleGlyLeuThrTyrIleSer----- 88
DB 681 -----CCCTGCTCTTCAGCATTCGCTGATGCTACAGCGAAAGAT 721
QY 89 -----LeuPheLeuPheTyrAlaProArgLysSerLysIlePheThrGlyTyr 104
DB 722 TTCAGAGAACAGATCATCCACCATGTGGCCACCATATTCTTCACGCTTTCTGCTTT 781
QY 104 PheMetLeuLeuGlyLeuGlyVala-----LeuGlyMetValMetProIleThrTyr 121
DB 782 GCCAATTACATCGGAGCTGGAGCTTAATCATGCTCTGATGATCGATTCGATTACCTG 841
QY 121 rLeuLeuAlaGlyLysSerHisArgValMetIleValGlyTyrIleCysAlaAlaIleAs 141
DB 842 -CTG-----GAGTCAGCCAAAGATGTTAACTAGCGCGGATGAGAGAACCTCGAACAA 894
QY 141 nVal-----AlaValAlaAlaAlaProLeuSerIleMetArgGlnValIleLysThrLysSe 160
DB 895 CACTTCATCATGCTTGTGCTGCTTTTATCATACCCGACGTGCTATC----- 943
QY 160 rValGlnPheMetProPheThrLeuSerLeuPheLeuThrLeuCysAlaThrMetTyrP 180
DB 944 -----CTGCCCTTCTGATC---CTGCATTCGACCCCTGTGTGATACCCACTGGAGCT 990
QY 180 ePheTyrGlyPhePheLysLysAspPheTyrIleAlaPheProAsnIleLeuGlyPheLe 200
DB 991 CTATCTGCTCTTCTGCTATTAATCTTCATTCATCATGATGAGGATTCACGCTGCT 1050
QY 200 u-----PheGlyIleValGlnMetLeuLeuTyrPheValTyrIleAspSe 215
DB 1051 GCATATCTTCTGGGCTTACTCTCATTTTGGCATGGCCACAGTTCTATA-----ACTGG 1104
QY 215 rLysArgIleAspAspGlnLysSerAspProValArgGlnAlaThrLysSerLysGlnG 235
DB 1105 AAGGCTGTGAAGATGAACGACGATGAC-----CGGAGAGAAACAGAGAGCTCAGAGGG 1158

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QY 235 yValGln 237
DB 1159 GGAGGAG 1165

RESULT 4
US-09-248-796A-12834
; Sequence 12834, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074.725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096.409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 12834
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-12834

Alignment Scores:
Pred. No.: 0.00647 Length: 759
Score: 107.00 Matches: 58
Percent Similarity: 42.92% Conservative: 42
Best Local Similarity: 24.89% Mismatches: 92
Query Match: 7.91% Indels: 42
DB: Gaps: 9

US-09-743-885a-1 (1-265) x US-09-248-796A-12834 (1-759)
QY 43 GlyTyrGlnAlaIleProTyrMetValAlaLeu-----PheSerAlaGlyLeuLeu----- 59
DB 49 GGGCTCAATCGGATATTTGCAATGTGTTCCTTGCTTCACCTGGGTTTGGCTGAT 108
QY 60 LeuTyrTyrAlaTyrLeuArgLysAsnAlaTyrLeuIleValSerIleAsnGlyPheGly 79
DB 109 GTAGATATATATAGACCGGTGCACTTTGGCTTGATGTTTCCATA----- 156
QY 80 CysAlaIleGlyLeuThrTyrIleSerLeuPheLeuPheTyrAlaProArgLysSerLys 99
DB 157 -----CTCAATCTTATCTATTTAGTTTACTATTCATGCTCATGCTACTATTCTCAAA 210
QY 100 IlePheThrGlyTyrLeuMetLeuGlyLeuGlyAlaLeuGlyMetValMetProIle 119
DB 211 AACTTTTACCTTCGGTAAATCAATTTA-----GTGGCGAGTTCAATTTCTTTGTG 261
QY 120 ThrTyrLeuLeuAlaGlyLysSerHisArgValMetIleValGlyTyrIleCysAlaAla 139
DB 262 TTTTATCTTCAGCCATGGAGCAATTCGACCGGTATTCCTTCGGAAGTTGTGA--- 318
QY 140 IleAsnValAlaValPheAlaAlaProLeuSerIleMetArgGlnValIleLysThrLys 159
DB 319 ---GATTATGGCAGTTACTCATCGCATCGCATCGCATCAAGGCTTTAATA----- 366
QY 160 SerValGlnPheMetProPheThrLeuSerLeuPheLeuThrLeuCysAlaThrMetTyr 179
DB 367 -----CCATTTACTTATTTCAACGAGTATTTGTTCTCTACTATTGGGA 411
QY 180 PhePheTyrGlyPhe-----PheLys-LysAsp 189
DB 412 TTATTTTGGGTTATAGCTTATTCACAAAGTCAGTAGTCGGAGATTCAAGTCAATCTT 471
QY 189 eTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuTyr 209
DB 472 TTACTCGACAGATTCAGAGTTGTGTCTATTTTACG-----ATTTCGCTTAA 519

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Oy 209 rPheValIYrLysAspSerLysArgIleAspAspGluLysSerAspProValArgGluI 229
Db 520 CCATTGGAAAAAATATCCGGTA-ACTGATCCAGTAAGTCTGACGCTGCTATTCGAATGC 578
Oy 229 aThrLysSerLysGluGlyValGlu-----IleIleIleAsnIleGluAspAs 245
Db 579 TGAAGTTCATCGTAGGCTATAGAAATAGATGCTCTTAAGATGTGCATCTGTGTGATTA 638
Oy 245 pAsnSerAspAsnAlaLeuGlnSerMetGluLysAsp 257
Db 639 TGAGCAACTGTTGGTTGGCTTCATCCGAGAAGAT 675

RESULT 5
US-09-270-767-8810
; Sequence 8810, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8810
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8810

Alignment Scores:
Pred. No.: 0.00945 Length: 503
Score: 103.50 Matches: 26
Percent Similarity: 47.87% Conservative: 19
Best Local Similarity: 27.66% Mismatches: 40
Query Match: 7.65% Indels: 9
DB: 4 Gaps: 1

US-09-743-885A-1 (1-265) x US-09-270-767-8810 (1-503)
Oy 133 ValGIYTPileCyAlaIleAlaIleAsnValAlaValPheAlaIleProLeuSerIleMet 152
Db 135 CTGGGAATCTTGATCATCCGCGCATCTCGTTGGATGCTGGCGCTCCCTCGTCGATCTG 194
Oy 153 ArgGlnValIleLysThrLysSerValGluPheMetProPheThrLysSerLeuPheLeu 172
Db 195 CCGAAATCATCATGAGAAGAGACCGAGGAGATCCGTTCCCGATTATCTTGGCCGT 254
Oy 173 ThrLeuCyAlaIleThreTrpPhePheTrpGlyPhePheLysLysAspPheTrpIleAla 192
Db 225 AATCTGGTGCGCATTTTCTCGACGCTGATGCCATCTTCATCAAGATATCTGTGATGCG 314
Oy 193 PheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuDeuTrpPheValTrp 212
Db 315 CTGCAAGATCTTTGTGCTGTGTCGTCGCGGCGGCGATTCACGTCCTCCATGTTCCGTA 374
Oy 213 -----LysAspSerLysArg 217
Db 375 CCGAACAAACCGGCTGCCGAGAACCCGACCGACAGCAAGAAG 416

RESULT 6
US-09-270-767-24092
; Sequence 24092, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24092

```

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; LENGTH: 503  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-770-767-24092  
  
Alignment Scores:  
Pred. No.: 0.000945 Length: 503  
Score: 103.50 Matches: 26  
Percent Similarity: 47.87% Conservative: 19  
Best Local Similarity: 27.66% Mismatches: 40  
Query Match: 7.65% Indels: 9  
DB: 4 Gaps: 1  
  
US-09-743-885A-1 (1-265) x US-09-270-767-24092 (1-503)  
QY 133 VALGIYTPIIECYALAlalaleanValAlavalPhalaAlarProleuseRilemeC 152  
::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 135 CTGGGAATGTGATACCGGCAGTCCTGTTTGAAATGGTGGCCCTCCCTGTCATCTG 194  
  
QY 153 ARGVIAIILElyThriySeserVaIgPheMetProPheThrPheLeupePheU 172  
::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 195 CCGAAATCATCGAGAAGAGCACGCCGAGAAATGCCCTTCCCATTACTTTGGCCGGT 254  
  
QY 173 ThrIeuCyBaIatHmetITrPhePheTyrgLyPhepheLyselYakSpheTyrlleaJa 192  
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 255 AATCTGGGCGCAATTTCTCTGGACGCGTAATGCCATCTCCATAAGAAATCTGATGATG 314  
  
QY 193 PheProAnillelueugLyPheuPhegylilevalGlmetLeuleutyryPheValTYr 212  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 315 CTGCAAAATCTTTTCTGCTGTCGTCGGAGCGCATTCACCTCTCCATGTTGGTATTAT 374  
  
QY 213 -----lysappserlysaRY 217  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 375 CCCAACAAACGGCTGCCGACAACCACCAAGACACAGAAAG 416  
  
RESULT 7  
US-09-790-988-1  
Sequence 1, Application US/09790988  
Patent No. 6632935  
GENERAL INFORMATION:  
APPLICANT: SHIGENOBU, SHUIJI  
APPLICANT: MATANABE, HIDEMI  
APPLICANT: HATORI, MASAHIRA  
APPLICANT: SAKAKI, YOSHIYUKI  
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
FILE REFERENCE: 081356/0159  
CURRENT APPLICATION NUMBER: US/09/790, 988  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: JP2000-107160  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 640681  
TYPE: DNA  
ORGANISM: Buchnera sp.  
US-09-790-988-1
```

```

Db      176224 TTTTAAAGATCAGCAGATATTACTTTACTTATTA-----AAACTAGCAAT 176274
Qy      43 GYTYRGlnAlaIleProTyRmetValAlaIleuPheSerAlaGly----- 57
Db      176275 GGTATAT-----GTGAGATGACGTACGTACATATATAGTATTAATTTATTTT 176328
Qy      58 ---LeuLeuLeuTyRValaTyRLeuAsglyAsnAla-----TyRleuIleVal 73
Db      176329 TTAATTAATGTTATTTTATTTTATTTAATAAAGACGTGTTTATTAATTAATTAATTT 176388
Qy      74 SerIle-----Aengly 77
Db      176389 GTTTTAAATAATATAATATTCTGTGATTAATAGTCATAGTGAATAAGCAATATA 176448
Qy      78 PheGlyCysAlaIleGluLeuThrTyRle-----SerleuPheLeuPhe 92
Db      176449 CGTGCATATGTTACTTCTTATTAATTAATATCCATTTTGTAGTGTGTTTCTTTT 176508
Qy      93 TyRAlaProArgLysSerLysIlePheThrGlyTyrPheMetLeuGluLeuGlyAla 112
Db      176509 TTTTCTCCTAGATGACATAATTTTCTCGCTGAGTTGCACATA-----TCAGGAATA 176562
Qy      113 LeuGlyMetValMetProIleThrTyRLeuLeuAlaGluGlySerHisArgValMetIle 132
Db      176563 ATTGCAACATTAATTAAGTGTAAATACAAATATTTTTCAGAAATAATATCATATTTTCAG 176622
Qy      133 Val-----GlyTyrIleCysAlaAlaIleAsn-----ValAlaValPheAla 146
Db      176623 ATTAGACATTACCTTAATGATGCAATTAATGTCATTAATGTCCTTCAGATTCAGATTTGCT 176682
Qy      147 AlaProLeuSerIleMetArgGlnValIleLysThrLysSerValGluPheMetProPhe 166
Db      176683 ATTGAAATTAACATTCCTGACCTGATGCTTATCATTAATATGCTTATTTTCTCTTTT 176742
Qy      167 ThrLeuSerLeuPheLeuThrLeuCysAlaThrMetTyrPhePheTyR----- 182
Db      176743 ---TATCATATATAAGCTATTAATATGTTCA-----TGGAATGAATAATTAATAAATGA 176793
Qy      183 GlyPhePheLysLysAspPheTyRleAlaPheProAsnIleGluGly-PheLeuPheG 202
Db      176794 GGAATTTTATTTATTTATTTATTTATGCTGTTTTCATGCTGATTAATGCTGTTTATTTT 176851
Qy      202 ylleValGlnMetLeuLeuTyRpheValTyR 212
Db      176852 -CTTGATCTTTTATTTTATTTTGTGTTT 176881

RESULT 8
US-09-134-000C-2036
; Sequence 2036, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2036
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2036

Alignment Scores:
Pred. No.: 0.00629 Length: 1188
Score: 101.50 Matches: 47
Percent Similarity: 43.33% Conservative: 44
Best Local Similarity: 22.38% Mismatches: 89

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Query Match: 7.50% Indels: 30
DB: 4 Gaps: 7

US-09-743-885a-1 (1-265) x US-09-134-000C-2036 (1-1188)
Qy      18 AsnIleValSerPheMetValPheLeuAlaProValProThrPheTyRlysIleTyRlys 37
Db      7 TCCGGGTGAAGACCTTATATGAGTCTCTTTTTCATTCCTCGTGG----- 51
Qy      38 ArgLysSerSerGluGlyTyRAlaIleProTyRmet-----ValAlaLeu 53
Db      52 CGGAAAAAGAAAAAGAACACATGTTGCTCCGTGAGTGTGTTGCTGACCTGCTTTATG 111
Qy      54 PreserAlaGlyLeuLeuLeuTyRValaTyRLeuAsglyAsnAlaTyRleuIleVal 73
Db      112 TTTCTTCTCA---TATGTTTATATTTAGAAATCATTCGTGGACACACCTCTTTTAAT 168
Qy      74 SerIleAenglyPheGlyCysAlaIleGluLeuThrTyRleSerleuPhe---LeuPhe 92
Db      169 CCATTTGCTTTTGTGGC-----TTGTTGGGCTCTTC 201
Qy      93 TyRAlaProArgLysSerLysIlePheThrGlyTyrPheMetLeuGluLeuGlyAla 112
Db      202 TACTTCAGAAAGAAAAAGCGCTTACTGAAATGGAACATTAATTAATATTTTCTGTGCTT 261
Qy      113 LeuGlyMetValMetProIleThr-----TyRleuLeuAlaGluGly 126
Db      262 CTAGGCACTTAATTTAGGATTAAGTCTGCAATTCGTACAAACACTCTTTTATACCTTA 321
Qy      127 SerHisArgValMetIleValGlyTyrIleCysAlaAlaIleAsnValAlaValPheAla 146
Db      322 GCAATTAATGCGCTGGTGCATATTTTATCGCTTGGCTTAAAGACTCATAGCTTAAT 381
Qy      147 AlaProLeuSerIleMetArgGlnValIleLysThrLysSerValGluPheMetProPhe 166
Db      382 ATTTTCTCTTAATGGAATCGGCTGCTGTATAGAGAAAGAAAGCGCTCATAGGAAC 441
Qy      167 ThrLeuSerLeuPheLeuThrLeuCysAlaThrMetTyrPhePheTyRlysIlePhePheLys 186
Db      442 TTGTTGACCTTGTGCTGCAATTTGCTTAACATTAATTAATTAATTAATTTCTTTT 501
Qy      187 LysAspPhe-----TyRleAla-PheProAsnIleGluGlyPheLeuPheGlyI 203
Db      502 CAATGTTGTTACAAACGTGCTCTCCCTTACCTTAACATTAATTTGCGCATTAATTTGACT 561
Qy      203 eValGlnMetLeuLeuTyRpheValTyR 212
Db      562 TATTTGCGCTTGTGTTTATTAATTTT 589

RESULT 9
US-09-199-737-1
; Sequence 1, Application US/09199737A
; Patent No. 6287788
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; APPLICANT: Branchek, Theresa A.
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; PRIOR FILING DATE: 1998-11-25
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Rat
US-09-199-737-1

Alignment Scores:

```



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Oy      171  theLeuThrIeuCYaLaIarhIheCTrPhePheThyGLY 183
Db      675  GGACGACGCGTATGT--TTCCATGTGGCCGCCGTGGGT 710

RESULT 11
US-09-058-333A-1
: Sequence 1, Application US/09058333A
: Patent No. 6368812
: GENERAL INFORMATION:
: APPLICANT: Bard, Jonathan A
: APPLICANT: Borowski, Beth
: APPLICANT: Smith, Kelly E
: TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/058,333A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 278 0400
: TELEFAX: 212 391 0525
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1280 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 63..1172
US-09-058-333A-1

Alignment Scores:
Pred. No.: 0.00815 Length: 1280
Score: 101.00 Matches: 46
Percent Similarity: 40.388 Conservative: 40
Best Local Similarity: 21.604 Mismatches: 67
Query Match: 7.46% Indels: 60
DB: 3 Gaps: 10

US-09-743-885A-1 (1-265) x US-09-058-333A-1 (1-1280)
Oy      9  LeuSerPheIILePheGlyLeuEngIyAaNIleValSerPheMetValPheLeuAlaPro 28
Db      138  CTCATCTTCCTCTGTGGCATGTGGGCAATGGCGCTGTGGCTGTGCTACTGACAGCCT 197
Oy      29  ValProThrPheTyrlYsIleTyrlYbArGlySeSerSerGluGly----- 43
Db      198  GGCCCAAGT-----GCCTGGCAGAGCAAGCAGTACACACAGATCTCTTCATCCTC 248
Oy      44  -----TyrGlnAlaIleProTyrlMetValAlaLeu 53
Db      249  AACTTGGCCGCTGGCCGACCTTGTCTTCATCTCTGTGTGCTGCTGCTCCATCCAGCAGCATC 300
Oy      54  PheSerAlaGlyLeuLeuLeuTyrlYrAlaTyrlYrLeuAlaGlybAaAlaTyrlYrLeuIleVal 73

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Db 309 TACACACGTGAGCCTGGCTCTTTGGGGGCTTTTCGTGTGACGAAGCGGTACATCTGCTCATC 368
 QY 74 SerileuenglyPheglyCysAlaIleGluLeuThrTyrIleSerleuPheleuPheTyr 93
 Db 369 TACCTCACCATGTATGCCAGACAGCTTCACCTGGCCGCGCTTCCTCCCTGGACAGATCACTG 428
 QY 94 Ala-----ProhylylseryIlePhe 101
 Db 429 GCTGTGGCGGACCCACCTGGCTCCAGAGCCCTGGCGACCCCGCGCAAGCGGCGCGCC 488
 QY 102 ThrGly-----TrpleumetleuengluLeuGlyAlaIleuGlyMetValmetProIle 119
 Db 489 GTGGGGCTCTGTGGCTG-----CTGGCGGCTCTCTTTTCGGCGCCCTACTA 536
 QY 120 ThrTyr-----LeuenuIaGluGlySerHisArgValMetIleValGlyTyrIleCys 137
 Db 537 AGCTATTACGACGAGCGTGGCTGACGGCGGCGCTCGACCTCTGCGCCCGCTGGGAGAC 596
 QY 138 Ala-----AlaIleasnValAlaValPheAlaIle-----ProleuSer 150
 Db 597 GGGCGGCGCGCGCGCTGGACGTGGCACCTTCGCGCGGGCTACTGCTGCGCGTGGC 656
 QY 151 IlemetArgIleValIlelysrThrlysserValGluPheMetProPheThrleuSerleu 170
 Db 657 GTGGTG-----ACCTTGCGCTAC 674
 QY 171 PheleuThrleuCysAlaThrmetTyrPhePheTyrGly 183
 Db 675 GGAGCGACGCTATGT--TTCCATGGGCGCGCGTGGGT 710
 RESULT 12
 US-09-328-352-1371
 ; Sequence 1371, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 1371
 ; LENGTH: 1389
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-1371
 Alignment Scores:
 Pred. No.: 0.0107 Length: 1389
 Score: 100.50 Matches: 59
 Percent Similarity: 39.92% Conservative: 40
 Best Local Similarity: 23.79% Mismatches: 91
 Query Match: 7.43% Indels: 59
 DB: 4 Gaps: 13
 US-09-743-885A-1 (1-265) x US-09-328-352-1371 (1-1389)
 QY 11 PheIlePheGlyLeuLeuGlyAlaIleValSerPheMetAlaPheleuAlaProValPro 30
 Db 670 TTTTTCATCGGAGCCCTTTTACCTATTGTAGTGTCGTAATTCGTGCGCTTATTTGGA 729
 QY 31 ThrPheTyrIleIleTyrIlysrGlysserSerGluGlyTyrIleAlaIleProTyrMet 50
 Db 730 ACT-----CAATCCTTTAAAGCGCTCAAGCAGAAACAGATCAGCGGAATACGAAATG 783
 QY 51 ValAlaIleuPhe-----SerAla 56
 Db 784 TTGGCTTATTAAACATTATCCTAAGAGAGCCTTCACTGATATTATTCCTAATCGTGT 843
 QY 57 GlyleuLeuTyrTyrIleTyrIleuAlaGlyIysAsnAlaTyrIleuIleValSerIleAsn 76

Dh 844 GGAATTGACTTTTAACTTACACTTATTACAGAAATATTAGTGAATACCTTCT 903
Qy 77 GlyPheGlyCys-----AlaIleGluLeuThrTyrlleSerleuPheLeuPheTyra 94
Dh 904 GGTTTTCAAGCCTGAGGCTACTACCAATTACCACTTAGCCTATTATCATCTTATATGTC 963
Qy 95 ProArgLysSerLysIlePheThrGlyTrrPheu-----Met 106
Dh 964 TTACAGCA-----TTGGCAGGTGCCCTTATCAGATCGAGTGGCCGTAACCCCTT 1014
Qy 107 LeuLeuGluLeuGlyAlaLeuGlyMetValMetProIleThrTyrlleLeuAlaGlu--- 125
Dh 1015 ATGATGCCCTTCGGGGTCAAGGTGTTTA-----TTCACTTAATTTTGTGGATACG 1068
Qy 126 -----GlySerHisArgValMetIleValGlyTrrIleCysAlaAlaIleAsnValAla 143
Dh 1069 CTTCGAACAACACTTAATCTAGCATCGATCTTCGTTATGT-----TTAGTGAGACTG 1122
Qy 144 ValPheAlaAlaProLeuSerIleMetArgGlnValIleuYsrThrLysSerValGluPhe 163
Dh 1123 ATTATGTAAACCGCTACACATCAATTAACTGCTAGTAA-----GCTGAACCTT 1173
Qy 164 MetProPheThrLeuSerLeuPhe-----LeuThrLeuCysAlaThrMetTrrPhe 180
Dh 1174 TTCCCTGC-ACATATTCGAGCTTTAGGTGTCGATACCTTAATGCAATTGGCAATACCTT 1232
Qy 181 -PheTyrgly-----PhePheLysAspPhe----- 189
Dh 1233 ATTTGGGTGACACCGAGTTTTCGATTAAGTTTAAAGAACCGGCGACGATCATG 1222
Qy 190 -TyrlleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeuTy 209
Dh 1293 GTTCTTATTTATTCCTCAGTATCATGATTTT-----ATTTCATTGCTGATTTA 1340
Qy 209 rPheValTyrlleAspSerLys 216
Dh 1341 TATTTTCATGAAGACACCAAG 1362

RESULT 13
US-09-543-1110
; Sequence 1110, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1110
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1110

Alignment Scores:
Pred. No.: 0.00795 Length: 864
Score: 99.00 Matches: 53
Percent Similarity: 38.46% Conservatives: 37
Best Local Similarity: 22.65% Mismatches: 89
Query Match: 7.32% Indels: 56
Gaps: 10

US-09-743-885A-1 (1-265) x US-09-543-681A-1110 (1-864)
Qy 18 AsnIleValSerPheMetValPheLeuAlaProValProThrPheTyrlleTyrllys 37
Dh 82 TCTATCTGCTGCTGCTGCTATATTACTAGCTGAGGTTTATTCCTCCCAAGTTGCTG 141
Qy 38 ArgLysSerSerGlyGlyTyrglnAlaIleProTyrrMet-----ValAlaLeuPhe 54

Dh 142 AGAAAGAGCAAAATGATACCGTGATTAAGCCCTGCTTTTTCGGTGGCTTGTG 201
Qy 55 SerAlaGlyLeuLeuLeuTyrrAlaTyrlleuArgLysAsnAlaTyrlleuIleValSer 74
Dh 202 ACCAGCTATCTCATTTAAATTTTGGATTTTCGCTCCACATAGCGGCAAAATCTCTCA 261
Qy 75 IleAsnGlyPheGlyCysAlaIleGluLeuThrTyrlleSerleuPheLeuPheTyra 94
Dh 262 CTCACCAATTTAGGGGGGTGTCAGTTTATGATGCTGCTATCATATGACCATTTGCT 321
Qy 95 ProArgLysSerLysIlePheThrGlyTrrPheMetLeu----- 107
Dh 322 TCCCGTGT-----AGAGCTGTGTTTGTCTGCTATTTATGCTTTTCC 369
Qy 108 -----LeuGluLeuGlyAlaLeuGlyMetValMetPro-----IleThrTy 121
Dh 370 ATAGTCAATCTCATTTATGCGGCTTG-----ATGCAAGTGAAGTTTGCACCCAC 420
Qy 122 LeuLeuAlaGluGlySerHisArgValMetIleValGlyTrrIleCysAlaAla----- 139
Dh 421 CTT-----GAAAGTAGACATCGCTCTTATTCATCA-TATTGGGCTTGCTTATTAACTTA 473
Qy 140 -----IleAsn-ValAlaValPheAlaAlaProLeuSerIleMetArgGlnValI 156
Dh 474 CGGCACCTTGTATATGCTGCTTTATATGCTTAACTAGCTGAGCTGACTATCAACT 533
Qy 156 elYsrThrLysSerValGluPheMetPro----- 165
Dh 534 AAAAATTAAGAAACTAAATTTTACCCACCAATGCCACATTAATGCAATTGACCTAA 593
Qy 166 ----PheThrLeuSer-----LeuPheLeuThrLeuCysAlaThrMe 178
Dh 594 AATGTTTCATATTAACCAAGTGGGGGTAGTATTACTGACATTAACCTTGTGACCGGCT 653
Qy 178 tTrrPhePheTyrglyPhePheLysAspPheTyrlleAlaPheProAsnIleLeuG 198
Dh 654 GTTATATATGATTAATATCTTTGTGTAAGAA-----AATATCATTA 695
Qy 198 yPheLeuPheGlyIleValGlnMetLeuLeuTyrrPheVal 211
Dh 696 ATCAATTTTCTTATTTATTCGCGTGTGCTACATCAT 735

RESULT 14
US-09-134-001C-1135
; Sequence 1135, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1135
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1135

Alignment Scores:
Pred. No.: 0.0123 Length: 1146
Score: 99.00 Matches: 52
Percent Similarity: 35.94% Conservatives: 40
Best Local Similarity: 20.31% Mismatches: 80
Query Match: 7.32% Indels: 84
Gaps: 12

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US-09-743-885a-1 (1-265) x US-09-134-001C-1135 (1-1146)
QY      15 LeuLeuGlyAsnIleValSerPheMet-----ValPheLeuAlaPro 28
Db      502 ATTATATCTAATTCAGTCATATATATACGCTTTTCATCTCAACGTGATTTATTAATA 561
QY      29 ValProThrPheTyrIleTyrIleTyrIleTyrIleTyrIleTyrIleTyrIlePro 48
Db      562 ATGGTCCTTTCTCTCGATATATATATGCTTAAGATCAAGAAAATTT-----ATCCCA 615
QY      49 TyrMetValAlaLeuPheSerAla----- 56
Db      616 GCATCGTAATAATTTTCAAGAGAACGTAAGTTTGTGTAGATTATTAAGAAC 675
QY      57 -----Gly 57
Db      676 TTAACTTCATTAAATCATATATTCAGAGTCAGTACGATGATCATCTTAGT 735
QY      58 LeuLeuLeuTyrTyrIleTyrIleTyrIleTyrIleTyrIleTyrIleTyrIleTyrIle 77
Db      736 ATTATTTTATATATAGTTAT----- 756
QY      78 PheGlyCysAlaIleGluLeuThrTyrIleSerLeuPheLeuPheTyrAlaProArgLys 97
Db      757 -----ACGATTTATAGGATTAACATATACACTTTTATAGTATTAATTCGCGCGTAGCT 810
QY      98 SerIleIle---PheThrGly---TyrPheMetLeuLeuGluLeuGluAlaLeuGlyMet 115
Db      811 AACTTAATACCATTTTATAGTTCATGCTGATATCTTTTGACCGGACGACGATACGATATT 870
QY      116 Val---MetProIleThrTyrIleLeuAlaGluGlySerHisArgValMetIleValGly 134
Db      871 ATTGATGCGCTTCAACTTTAT----- 894
QY      135 TrpIleCysAlaAlaIleAsnValAlaValPheAlaAlaProLeu---SerIleMet 152
Db      895 TGGGATATGATC-----GTAACATTAATCGCACACACATGTAAGGTAACGTGATA 945
QY      153 ArgGlnValIleLeuThrIleSerValGluPheMetProPheThrIleuSerIleuPheLeu 172
Db      946 ACTCCTAAGCTAATGGGTAATATCATTAAGCATTCATTAATTAATTAATGTTGATATA 1005
QY      173 ThrLeuCysAlaIleThrPhePheTyrGlyPhePheIleValSerPheTyrIleAla 192
Db      1006 CTTCGACGCTGAGATTTGGGTGTTT-----ACACTCATTTCTTGTGCA 1050
QY      193 PheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeuTyrPheValTyr 212
Db      1051 GTTCCA-----TTATACGCTGTATCAAAACATTAGAGACACATTTT 1095
QY      213 LysAspSerLysArgIleAspAspGluLysSerAspProValArgGlu 228
Db      1096 AATATATCGTCAACGTATTTGCGATAAAGAACAGTAATGTTAAAGAT 1143

RESULT 15
US-09-711-164-238
; Sequence 238, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Foresyth, R. Allyn
; APPLICANT: Ohlson, Karl
; APPLICANT: Zwickind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
; FILE REFERENCE: ELTRA-006A
; CURRENT APPLICATION NUMBER: US/09/711,164
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 1704
; TYPE: DNA

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; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1704)
; US-09-711-164-238

Alignment Scores:
Pred. No.: 0.026 Length: 1704
Score: 98.50 Matches: 56
Percent Similarity: 37.55% Conservative: 48
Best Local Similarity: 20.22% Mismatches: 86
Query Match: 7.28% Indels: 87
DB: Gaps: 14

US-09-743-885a-1 (1-265) x US-09-711-164-238 (1-1704)
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QY      43 GlyTyrGlnAlaIleProTyrMetValAlaLeuPhe-----SerIleGlyLeuLeu 59
Db      61 ACGATCTGGCAATTTTCTATATATTCCTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 120
QY      60 LeuTyrTyr-----AlaTyrIleuArgLysAsnAlaTyrIleuIleValSerIleAsn 76
Db      121 TTTCATATTTTACCGCTGCTTACAAAAGTAATTGTTAT----- 162
QY      77 GlyPheGlyCysAlaIleGluLeuThrTyrIleSerLeuPheLeuPheTyrAlaProArg 96
Db      163 -----GAATGTCATCAAGAACTTGATTCATTAACAATTTTATTTT----- 204
QY      97 LysSerLysIlePheThrGlyTyrPheMetLeuLeuGluLeuGluAlaLeuGlyMetVal 116
Db      205 -----TCACTGAAACCCGATGTAACCTC-----ATATCTCTGTGTGAGATTTT 249
QY      117 MetProIleThrTyrIleuLeuAlaGluGlySerHisArgVal----- 130
Db      250 ATTGCATCTGTTTATA-----CAGCATAGAAATTAAGCTTATTAACATTA 297
QY      131 MetIleValGlyTrpIleCysAlaAlaIle----- 140
Db      298 TTACGATTAACATGATTTGTAATCAATTAACAGATGCGCTTAATACACGCTTAGAC 357
QY      141 AsnValAlaValPheAlaAlaProLeuSerIleMetArgGlnValIleLeuThrLysSer 160
Db      358 AATATAGCCATGAATATATTTGTTAAATATATATATATATATCTT----- 402
QY      161 ValGluPheMetProPheThrIleuSerLeuPheLeuThrIleuCysAlaIleThrMetTrpPhe 180
Db      403 -----TTTGGGCGCATTTTATTTGTCATCTGTTTATGTTATCAAAATCCCTCTTTC 456
QY      181 PheTyrGlyPhePheIleValSerPheTyrIleAlaPheProAsnIleLeuGlyPheLeu 200
Db      457 CACCTTAATGAAGTAATAACAT-----ATTCAATGATTTATATGCGCAATG 501
QY      201 PheGlyIleValGlnMetLeu-----LeuTyrPheVal 211
Db      502 ATTCATTAATGTTCCCAATTAATATAGCCATATCAATACCGCTGTTATATTTATTTATTT 561
QY      212 TyrLysAspSerLysArgIleAspAspGluLysSerAspProValArgGluAlaThrLys 231
Db      562 TTT----- 564
QY      232 SerIleGluGlyValGluIleIleIleAsnIleGluAspAspAsnSerAspAsnAla--- 250
Db      565 GCCCGACGCGGTAGATGATGATGATATAT---TCGAAGGTTCAAGCATCGCATAT 621
QY      251 -----LeuGlnSerMetGluLysAspPheSerArgLeuArgThrSerLys 265
Db      622 GTAGGTATAAAGATATAGAGAAATCATTTGGGTTTAAATGATTAATAA 672

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Mon Dec 27 09:34:22 2004

us-09-743-885a-1.rni

Page 10

Search completed: December 24, 2004, 22:23:41
Job time : 232 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 24, 2004, 20:44:17 ; Search time 589 Seconds
(without alignments)
2361.794 Million cell updates/sec

Title: US-09-743-885a-1

Perfect score: 1353
Sequence: 1 MAQRAADLSFIFGLGNIV.....NSDNALQSMEXKDFSLRTSK 265

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO_epool_p/US09743885/runat_23122004_165258_9626/app_query.fasta_1.455
-DB=N Geneseq_23Sep04 -QFMT=faetap -SUFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosumm62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODELOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09743885@CGN_1_1.885@runat_23122004_165258_9626 -NCPU=6 -ICPU=3
-NO_WMAP -LANG=QUEYRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WAPN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq_23Sep04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
5: geneseqn20028:*
6: geneseqn20038:*
7: geneseqn20048:*
8: geneseqn20058:*
9: geneseqn20068:*
10: geneseqn20078:*
11: geneseqn20088:*
12: geneseqn20098:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1205	AAZ35493	AAZ35493 Petunia n
2	1353	100.0	1205	AAZ50200	AAZ50200 Petunia h
3	1309	96.7	847	AAZ55498	AAZ55498 Petunia n
4	1309	96.7	847	AAZ50207	AAZ50207 Clone RC8
5	704.5	52.1	900	AAZ47558	AAZ47558 Arabidops
6	703.5	52.0	902	AAZ40321	AAZ40321 Arabidops

7	623.5	46.1	879	6	ABZ13458	Abz13458 Arabidops
8	623.5	46.1	1263	3	AAZ34308	AAZ34308 Arabidops
9	622	46.0	870	12	ADN73900	Adn73900 Thale cre
10	622	46.0	1177	3	AAZ51633	AAZ51633 Arabidops
11	622	46.0	1189	3	AAZ41129	AAZ41129 Arabidops
12	621.5	45.9	1219	3	AAZ49337	AAZ49337 Arabidops
13	621.5	45.9	1221	3	AAZ39463	AAZ39463 Arabidops
14	618	45.7	985	3	AAZ46920	AAZ46920 Arabidops
15	590	43.6	1252	3	AAZ47147	AAZ47147 Arabidops
16	564.5	41.7	1159	3	AAZ33952	AAZ33952 Arabidops
17	564.5	41.7	1159	3	AAZ47391	AAZ47391 Arabidops
18	548.5	40.5	569	9	AAZ13033	AAZ13033 DNA clone
19	486	35.9	651	9	AAZ13113	AAZ13113 DNA clone
20	461	34.1	675	9	AAZ13102	AAZ13102 DNA clone
21	447	33.0	974	12	ADN47592	Adn47592 Polynucle
22	447	33.0	990	3	AAZ37819	AAZ37819 Arabidops
23	429	31.7	1163	12	ADN47593	Adn47593 Polynucle
24	417	30.8	522	9	AAZ13056	AAZ13056 DNA clone
25	417	30.8	599	9	AAZ13064	AAZ13064 DNA clone
26	417	30.8	602	9	AAZ13077	AAZ13077 DNA clone
27	417	30.8	634	9	AAZ13076	AAZ13076 DNA clone
28	407	30.1	582	9	AAZ13025	AAZ13025 DNA clone
29	406.5	30.0	555	9	AAZ13060	AAZ13060 DNA clone
30	406.5	30.0	603	9	AAZ13078	AAZ13078 DNA clone
31	406.5	30.0	625	9	AAZ13062	AAZ13062 DNA clone
32	406.5	30.0	632	9	AAZ13080	AAZ13080 DNA clone
33	406.5	30.0	656	9	AAZ13087	AAZ13087 DNA clone
34	405.5	30.0	661	9	AAZ13030	AAZ13030 DNA clone
35	405.5	30.0	668	9	AAZ13022	AAZ13022 DNA clone
36	403.5	29.8	933	3	AAZ50752	AAZ50752 Arabidops
37	401.5	29.7	439	9	AAZ13058	AAZ13058 DNA clone
38	401.5	29.7	551	9	AAZ13082	AAZ13082 DNA clone
39	401.5	29.7	623	9	AAZ13068	AAZ13068 DNA clone
40	401.5	29.7	638	9	AAZ13086	AAZ13086 DNA clone
41	401.5	29.7	639	9	AAZ13098	AAZ13098 DNA clone
42	401.5	29.7	644	9	AAZ13084	AAZ13084 DNA clone
43	401.5	29.7	650	9	AAZ13097	AAZ13097 DNA clone
44	400.5	29.6	673	9	AAZ13032	AAZ13032 DNA clone
45	400.5	29.6	937	3	AAZ38614	AAZ38614 Arabidops

ALIGNMENTS

RESULT 1	AAZ35493	
ID	AAZ35493	standard; cDNA; 1205 BP.
XX		
AC	AAZ35493;	
XX		
DT	15-SEP-2003	(revised)
DT	11-APR-2000	(first entry)
XX		
DE	Petunia nectary-specific NECL cDNA.	
XX		
KW	NECL; nectary; nectar; transgenic plant; honey; ds.	
XX		
OS	Petunia x hybrida.	
XX		
FN	Key	Location/Qualifiers
FT	CDS	79..876
FT		/*tag= a
XX		
PN	EP974667-A1.	
XX		
PD	26-JAN-2000.	
XX		
PF	16-JUL-1998;	98EP-00202375.
XX		
PR	16-JUL-1998;	98EP-00202375.
XX		
PA	(CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.	
XX		
PI	Creemers J, Angenent GC, Kater MM;	

XX WPI; 2000-108400/10.
 DR P-PSDB; AAY58647.
 XX Novel DNA sequences used to produce modified honey, the metabolites of
 PT which can be isolated and purified.
 XX Claim 2; Page 16; 56pp; English.
 XX The present sequence is that of Petunia hybrida strain W15 NECL cDNA, as
 CC produced from 2 overlapping partial clones (see AA235497-98) obtained by
 CC differential display RT-PCR and RACE PCR. The NECL gene encodes a 265-
 CC amino acid protein (see AAY58647). NECL is highly expressed in the
 CC nectaries of petunia and weakly expressed in the stem. The present
 CC invention provides a method for producing recombinant proteins in honey.
 CC The honey is manufactured by insects, preferably honeybees, that collect
 CC the nectar of transgenic plants. The NECL gene and its promoter (see
 CC AA235496) can be utilized in expression cassettes for the production of
 CC transgenic plants that produce a protein of interest in their nectar. The
 CC function of NECL has not yet been determined. (Updated on 15-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 1205 BP; 374 A; 219 C; 229 G; 383 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.8e-143 Length: 1205
 Score: 1353.00 Matches: 265
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
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 QY 1 MetAlaGlnLeuArgAlaAspAspLeuSerPheIlePheGlyLeuGlyAsnIleVal 20
 DB 79 ATGGCGCAATTCAGTCTGCTGATGACTTGTCTTTCATATTTGGCTTTGGTAATATTGTA 138
 QY 21 SerPheMetValPheLeuAlaProValProThrPheTyrLysIleTyrLysArgLysSer 40
 DB 139 TCATTCAATGGTCTCTTCAGCACCCGTGCACAACTTTTACAAATATATATAAGAAATCA 198
 QY 41 SerGlnGlyTyrGlnAlaIleProTyrMetValAlaLeuPheSerAlaGlyLeuLeuLeu 60
 DB 199 TCAGAAAGAAATCAAGCAATACCATATATGTATGACACTGTTCAGCGCGACTATTGCTA 258
 QY 61 TyrTyrAlaTyrLeuArgLysAsnAlaTyrLeuIleValSerIleAsnGlyPheGlyCys 80
 DB 259 TATTATGCTTATCTCAGAGAGAAATGCTTATCTTATGCTGACGATTAATGGCTTGGATGT 318
 QY 81 AlaIleGlnLeuThrTyrIleSerLeuPheLeuPheTyrAlaProArgLysSerLysIle 100
 DB 319 GCCATTGAATTAACATATATCTCTCTTTTACGGGCCCAAAAGTCTAAAGATT 378
 QY 101 PheThrGlyTyrPheMetLeuLeuGlnLeuGlyAlaLeuGlyMetValMetProIleThr 120
 DB 379 TTCACAGGGGCGCGATGCTCTTGAATGGGAGCCCTAGGAATGGATGCCAATTACT 438
 QY 121 TyrLeuLeuAlaGlnLysSerHisArgValMetIleValGlyTyrPheCysAlaAlaIle 140
 DB 439 TATTATTAGAGAGAGGCTCACTATAGATGATGATGATGGATGGATTTGTGCGCTATC 498
 QY 141 AsnValAlaValPheAlaAlaProLeuSerIleMetArgIleValIleLysThrLysSer 160
 DB 499 AAGGTCTGCTTGTGCTGCTCTTTAAGCATCATAGGCGCAAGTAATAAAAACAAGT 558
 QY 161 ValGlnPheMetProPheThrLeuSerLeuPheLeuThrLeuCysAlaIleMetTyrPhe 180
 DB 559 GTAGAGTTCAATGCGCTTCACTTATCTTGTCTCTCACTGCTGCTGCTATGCTGTTT 618
 QY 181 PheTyrGlyPhePheLysLysAspPheTyrIleAlaPheProAlaIleLeuGlyPheLeu 200
 DB 619 TTCTATGGGTTTTCAGAGAGGACTTTTACATTCGTTTCCAAATATATACGGGCTTTCTA 678

QY 201 PheGlyIleValGlnMetLeuLeuTyrPheValTyrLysAspSerLysArgIleAspAsp 220
 DB 679 TTCGGAATGCTTCAATGCTATATATTTGTTTACAGGATTCAAAGAGAAATAGATGAT 728
 QY 221 GlnLysSerAspProValArgIleAlaThrLysSerLysGlnGlyValGlnIleIle 240
 DB 739 GAAAAATCTGATCTCTTCGAGAGGCTACAAATCAAAAGAGGTGTAGAAATCATTTATC 798
 QY 241 AsnIleGlnAspAspAsnSerAspAsnAlaLeuGlnSerMetGlnLysAspPheSerArg 260
 DB 799 AACATTGACATATATATTTCTGATTAACGATTCATGCAATGAGAGAAATTTTCCAGA 858
 QY 261 LeuArgThrSerLys 265
 DB 859 CTCGCGACATCAAAA 873
 RESULT 2
 AA250200
 ID AA250200 standard; cDNA; 1205 BP.
 XX
 AC AA250200;
 XX
 DT 15-SEP-2003 (revised)
 DT 17-MAY-2000 (first entry)
 DE
 XX
 DE Petunia hybrida nectary-specific protein NECL cDNA.
 XX
 KM NECL; nectary-specific protein; metabolite; recombinant protein;
 KM transgenic plant; nectar; honey; insect; bee; pharmaceutical; enzyme;
 KM biotect; antioxidant; food additive; ss.
 XX
 OS Petunia x hybrida.
 XX
 FH Key Location/Qualifiers
 FT CDS 79..876
 FT /tag= a
 FT /product= "NECL protein"
 FT
 XX
 MO200004176-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 15-JUL-1999; 99MO-ML000453.
 PF
 XX 16-JUL-1998; 98BP-00202375.
 PR 14-DEC-1998; 98BP-00204215.
 PR
 XX (CPRO-) CPRO-DIO CENT PLANTENVEREDELINGS REPROD.
 PA
 XX Creemers J, Angenent GC, Kater MM;
 PI WPI; 2000-182438/16.
 XX P-PSDB; AAY44803.
 DR
 DR
 DR
 XX
 PT New DNA encoding Petunia hybrida nectary-specific proteins, useful for,
 PT e.g. producing modified honey.
 XX
 PS Claim 8; Page 42; 93pp; English.
 XX
 XX The present sequence is a cDNA encoding nectary-specific protein NECL. It
 CC was isolated from nectaries of Petunia hybrida strain W15 using mRNA
 CC Differential Display system. NECL resembles membrane protein and is
 CC strongly expressed in the nectaries of P. hybrida. A DNA sequence from
 CC the promoter region upstream of nectary-specific expressed sequence e.g.
 CC NECL and FBP15 DNA is used in a recombinant DNA construct comprising a
 CC DNA encoding a metabolite preferably recombinant protein, a DNA encoding
 CC a signal peptide that targets the recombinant protein to the nectar and
 CC optionally a signal sequence functional in plants for the transcription
 CC termination and polyadenylation of an RNA molecule. The DNA construct is
 CC useful for producing transgenic plants which excrete recombinant proteins
 CC in its nectar. The nectar is processed into honey by insects (preferably
 CC bees) and the desired protein is easily recovered from it. The

CC recombinant proteins are useful for pharmaceutical purposes, as enzymes
CC for bioassays and antioxidants for food additives. (Updated on 15-SEP-2003
CC to standardise OS field)

XX Sequence 1205 BP; 374 A; 219 C; 229 G; 383 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 1353.00	1205	265	0	0	0	0
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 100.00%						
DB: 3						

US-09-743-885a-1 (1-265) x AA250200 (1-1205)

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QY 1 MetAlaGlnLeuArgLaaApApLeuSerPheIlePheGlyLeuLeuGlyAenIleVal 20
DB 79 ATGGCCCAATTACGCTGCTGATGACTTGTCTTTCATATTGGCTTCTGGTATATTGTA 138
QY 21 SerPheMetValPheLeuAlaProValProThrPheTyrIleValIleTyrIleValSer 40
DB 139 TCATTATGATGCTCTTCCAGACCCGCGCCAACTTTTACAAATATATATAAGAAATCA 198
QY 41 SerGluGlyTyrGlnAlaIleProTyrMetValAlaLeuPheSerAlaGlyLeuLeu 60
DB 199 TCAGAGGATATACGACATACCATATATAGTAGCACTGTTCCGCCCGGACATATTGCTA 258
QY 61 TTTTATATATyrLeuArgLysAenAlaTyrLeuIleValSerIleAenGlyPheGlyCys 80
DB 259 TATTATGCTTATCTCAGAAAGAAATGCTTATCTATGTCAGCATTTATAGCTTTGGATGT 318
QY 81 AlaIleGlnLeuThrTyrIleSerLeuPheLeuPheTyrAlaProArgLysSerIle 100
DB 319 GCCATTGAATTACATATATCTCTCTGTTTCTCTTTTACCCGCCCAAGTCTTAAGATT 378
QY 101 PheThrGlyTyrLeuMetLeuLeuGlyValAlaLeuGlyMetValMetProIleThr 120
DB 379 TTCACAGGGTGGCTGCTCTTGAATTTGGAGCCCTTACGAATGGTATGCTCAATTACT 438
QY 121 TTTTLeuLeuAlaGlyLysSerIleAenValMetIleValGlyTyrIleCysAlaIle 140
DB 439 TATTATTTAGCAGAAAGGCTACATAGAGTATGATGATGATGATGATGATGATGATGATG 498
QY 141 AenValAlaValPheAlaAlaProLeuSerIleMetArgGlnValIleTyrThrLysSer 160
DB 499 AATGTTGCTGCTCTTCTCTCTCTTAAAGCATATGAGGCAAGTATATAAACAAGAGAT 558
QY 161 ValGluPheMetProPheThrLeuSerLeuPheLeuThrLeuCysAlaIleThrMetTyrPhe 180
DB 559 GTAGAGTTTCATGCTCTTACCTTATCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 181 PheTyrGlyPhePheLysLysAenPheTyrIleAlaPheProAenIleLeuGlyPheLeu 200
DB 619 TTTCTATGGGTTTTCAGAAAGGACTTTTACATTCGCTTCAAAATATATCTGGGCTTTCTA 678
QY 201 PheGlyIleValGlnMetLeuLeuTyrPheValTyrLysAenSerLysArgIleAenPhe 220
DB 679 TTGGAATGCTTCAAAATGCTATATATTTTGTTTTACAAAGATTCAAAGAAATAGATGAT 738
QY 221 GluLysSerAenProValArgGlyAlaThrLysSerIleGlyValIleIleIle 240
DB 739 GAAATATCTGATCTGTTTCAGAAAGCTACAAATTCAAAGAGGTGTAAGAAATCATATATC 798
QY 241 AenIleGluAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 260
DB 799 AACATTGAGAGATGATATCTGATTAACGATTCGATTCGATTCGATTCGATTCGATTCGAT 858
QY 261 LeuArgThrSerLys 265
DB 859 CTGCGGACATCAAAA 873
RESULT 3

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AA235498
ID AA235498 standard; cDNA; 847 BP.
XX
XX AA235498;
AC
XX 15-SEP-2003 (revised)
DT 11-APR-2000 (first entry)
XX
DE Petunia nectary-specific NECL cDNA partial clone Rc8.
XX
XX NECL; nectary; nectar; transgenic plant; honey; ds.
XX
XX Petunia x hybrida.
OS
XX EP974667-A1.
XX
XX 26-JUN-2000.
XX
XX 16-JUL-1998; 98BP-00202375.
XX
XX 16-JUL-1998; 98BP-00202375.
XX
XX (CPRO-) CPRO-DIO CENT PLANTENVERDELINGS REPROD.
XX
XX Creemers J, Angenent GC, Kater MM;
XX
XX WPI, 2000-108400/10.
XX
XX Novel DNA sequences used to produce modified honey, the metabolites of
XX which can be isolated and purified.
XX
XX Example 1; Fig 3; 56pp; English.
XX
XX The present sequence is that of clone Rc8, a 5' cDNA clone obtained from
XX CC Petunia hybrida strain W15 by RT-PCR. Clone Rc8 and overlapping clone
XX CC DD18a (see AA235497), obtained by differential display RT-PCR, were used
XX CC to generate a full-length cDNA (see AA235493) of a gene termed NECL. The
XX CC NECL gene is highly expressed in the nectaries of petunia and weakly
XX CC expressed in the stemens. The present invention provides a method for
XX CC producing recombinant proteins in honey. The honey is manufactured by
XX CC insects, preferably honeybees, that collect the nectar of transgenic
XX CC plants. The NECL promoter (see AA235496) can be utilised in expression
XX CC cassettes for the production of transgenic plants that produce a protein
XX CC of interest in their nectar. (Updated on 15-SEP-2003 to standardise OS
XX CC field)
XX
XX Sequence 847 BP; 249 A; 157 C; 172 G; 269 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
Pred. No.: 3 95E-138 Length: 847
Score: 1309.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.75% Indels: 0
DB: 3 Gaps: 0
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QY 21 SerPheMetValPheLeuAlaProValProThrPheTyrIleValIleTyrIleValSer 40
DB 139 TCATTATGATGCTCTTCCAGACCCGCGCCAACTTTTACAAATATATATAAGAAATCA 198
QY 41 SerGluGlyTyrGlnAlaIleProTyrMetValAlaLeuPheSerAlaGlyLeuLeu 60
DB 199 TCAGAGGATATACGACATACCATATATAGTAGCACTGTTCCGCCCGGACATATTGCTA 258
QY 61 TTTTATATATyrLeuArgLysAenAlaTyrLeuIleValSerIleAenGlyPheGlyCys 80
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QY 81 AlallegleuThrTyrIleSerleuPheleuPheTyrAlaProAlglySerIle 100
D 319 GCCATTGAATTAACATATATCTCTCTTTTACAGGCCCAAGAACTTAAGATT 378
QY 101 PheThrGlyTTPleuMetleuGluLeuGlyAlaLeuGlyMetValMetProIleThr 120
D 379 TTCACAGGGTGGCTGATGCTCTTGAATTTGGAGCCCTTAGAAATGGATGCCAATTACT 438
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D 439 TATTATTAGCAGAAGGCTCATAGACTGATGATAGTGGATGGATTGTGCGACTATC 498
QY 141 AsnValAlaValPheAlaAlaProleuSerIleMetArgGlnValIleYsThrLysSer 160
D 499 AATGTGCTGCTTTGGCTGCTCTTTAAGCATCATGAGGCAAGTAATAAACAAGAGT 558
QY 161 ValGluPheMetProPheThrleuSerleuPheleuThrleuCysAlaIleMetTTPhe 180
D 559 GTAGAGTTCATGCTTCACTTATCTTGTTCCTCACTCTGTGCGCATATGTGTGTT 618
QY 181 PheTyrGlyPhePheLysLysAspPheTyrIleAlaPheProAlaIleleuGlyPheleu 200
D 619 TTCATAGGCTTTTCAAGAGGACTTTTACATTCGCTTCCAAATATATGCGCTTTCTA 678
QY 201 PheGlyIleValGlnMetleuLeuTyrPheValTyrLysAspSerLysArgIleAspAsp 220
D 679 TTCGGAATCGTTCAATGCTATATATTTGTTACAAAGATCAAGAGAAATGATGAT 738
QY 221 GluLysSerAspProValArgGlnAlaThrLysSerLysGlyValGlnIleIle 240
D 739 GAAATAATCTGATCTGTTCGAGAAAGCTACAAATAAGAGGTGTAAGAAATCATATATC 798
QY 241 AsnIleGluAspAspAsnSerAspAsnAlaIleuGlnSerMetGluLys 256
D 799 AACATTGAAGATGATATTTCTGATACCGCATTCGATCGAGGAAG 846
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ID AAZ50207 standard; DNA; 847 BP.
AC AAZ50207;
XX
XX 15-SEP-2003 (revised)
XX 17-MAY-2000 (first entry)
DE Clone RC8 for cloning P. hybrida NEC1 gene.
XX
XX NEC1; nectary-specific protein; metabolite; recombinant protein;
XX transgenic plant; nectar; honey; insect; bee; pharmaceutical; enzyme;
XX biotect; antioxidant; food additive; clone RC8; ds.
XX
XX Petunia x hybrida.
XX
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XX /*tag= a
XX /bound_moiety= "Prat 129 primer"
XX /note= "Prat 129 is used with primer prat 122 to amplify
XX the coding region of NEC1 cDNA."
XX
XX WO200004176-A1.
XX
XX 27-JAN-2000.
XX
XX 15-JUL-1999; 99WO-NL000453.
XX
XX 16-JUL-1998; 98EP-00202375.
XX 14-DEC-1998; 98EP-00204215.
XX
XX (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX Creemers J, Angenent GC, Kater MM;
PI
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XX WPI; 2000-182438/16.
DR
XX New DNA encoding Petunia hybrida nectary-specific proteins, useful for,
PT e.g. producing modified honey.
XX
XX Example 1; Fig 3; 93pp; English.
XX
XX The patent discloses a recombinant DNA construct comprising a DNA
CC sequence from the promoter region upstream of nectary-specific expressed
CC sequence e.g. NEC1 and FRP15 DNAs, a DNA encoding a metabolite preferably
CC recombinant protein, a DNA encoding a signal peptide that targets the
CC recombinant protein to the nectar and optionally a signal sequence
CC polyaenylation of an RNA molecule. The DNA construct is useful for
CC producing transgenic plants which excrete recombinant proteins in its
CC nectar. The nectar is processed into honey by insects (preferably bees)
CC and the desired protein is easily recovered from it. The recombinant
CC proteins are useful for pharmaceutical purposes, as enzymes for biotests
CC and antioxidants for food additives. The present DNA sequence is that of
CC clone RC8 obtained by 5' RACE PCR of cDNA derived from nectaries of P.
CC hybrida flowers. The overlapping sequences of this clone and a 3' cDNA
CC clone DP18a were used to isolate the full length cDNA of P. hybrida NEC1
CC gene which is strongly expressed in nectaries. (updated on 15-SEP-2003 to
CC standardise OS field)
XX
XX SQ Sequence 847 BP; 249 A; 157 C; 172 G; 269 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3.95e-138 Length: 847
XX Score: 1309.00 Matches: 256
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 96.75% Indels: 0
XX DB: 3 Gaps: 0
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D 79 ATGGCGCAATTAGCTGTGATGACTGTCTTTCATATTTGGCTTCTGTGTAATATTGTA 138
QY 21 SerPheMetValPheleuAlaProValProThrPheTyrLysIleTyrLysArgLysSer 40
D 139 TCATTCATGCTCTCTCTACGACCCGTCGCAACATTTTACAAATATATAAAGGAATCA 198
QY 41 SerGluGlyTyrGlnAlaIleProTyrMetValAlaIleuPheSerIleGlyleuLeu 60
D 199 TCGAAGAGATATCAAGCAATATCATATATGTGACACTGTTCAGCGCGGACTATATGCTA 258
QY 61 TyrTyrAlaTyrleuArgLysAsnAlaTyrLeuIleValSerIleAsnGlyPheGlyCys 80
D 259 TATTATGCTTATCTCAGGAAGATGCCATCTATCTGTCAGCATTAATGCTTTGATATG 318
QY 81 AlallegleuThrTyrIleSerleuPheleuPheTyrAlaProAlglySerIle 100
D 319 GCCATTGAATTAACATATATCTCTCTTTTACAGGCCCAAGAACTTAAGATT 378
QY 101 PheThrGlyTTPleuMetleuGluLeuGlyAlaLeuGlyMetValMetProIleThr 120
D 379 TTCACAGGGTGGCTGATGCTCTTGAATTTGGAGCCCTTAGAAATGGATGCCAATTACT 438
QY 121 TyrleuAlaIagluGlySerHisArgValMetIleValGlyTTPleCysAlaAlaIle 140
D 439 TATTATTAGCAGAAGGCTCATAGACTGATGATAGTGGATGGATTGTGCGACTATC 498
QY 141 AsnValAlaValPheAlaAlaProleuSerIleMetArgGlnValIleYsThrLysSer 160
D 499 AATGTGCTGCTTTGGCTGCTCTTTAAGCATCATGAGGCAAGTAATAAACAAGAGT 558
QY 161 ValGluPheMetProPheThrleuSerleuPheleuThrleuCysAlaIleMetTTPhe 180
D 559 GTAGAGTTCATGCTTCACTTATCTTGTTCCTCACTCTGTGCGCATATGTGTGTT 618
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QY 181 PheTYGlyPhePheIysLysAspPheTYrIleAlaPheProxeniIleuGlyPheLeu 200
Db 619 TTCATAGGGTTTTCAGAAAGACITTTACATTCGCTTCCAATATACCTGGCTTTCTA 678
QY 201 PheGlyIleValGlnMetLeuIleTYrPheValTYrIysAspSerIysaTYrIleAspAsp 220
Db 679 TTCGAATCGTTCAAATGCTATTATATTTGTTTACAGAGATTCAAGAGAAATAGATGAT 738
QY 221 GlnLysSerAspProValArgGluAlaThrLysSerIleGlnGlyValGluIleIle 240
Db 739 GAAATAATCGATCTCTTCAGAGAGCTACAAATAACAAAGAGCTGAGAAATCATTATC 798
QY 241 AenIleGluAspAspAsnSerAspAsnAlaLeuGlnSerMetGluLys 256
Db 799 AACATTGAAGATGATTAATTTCTGATTAACGCTTCAGCTCCATGAGAGAG 846
RESULT 5
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XX AAC47558;
AC
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54267.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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KM Hybridization assay; Genetic mapping; Gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

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Alignment Scores:

Pred. No.:	1.23e-69	Length:	902
Score:	703.50	Matches:	136
Percent Similarity:	74.49%	Conservative:	48
Best Local Similarity:	55.06%	Mismatches:	62
Query Match:	52.00%	Indels:	1
	3	Gaps:	1

US-09-743-885A-1 (1-265) x AAC40321 (1-902)

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QY 24 ValPheLeuAlaProValProThPheTyLys1LeTyTyLysArgLysSerSerGluGly 43
Db 111 GTGTTCTTGTCACAGTCGCAAGCTTTTATGCGATATACAAAGAAATCATCAAAAGG 170
QY 44 TyrcGlnAla1leP-cotyrmcValAlaLeuPheSer1ag1LeuLeuLeuTyTyTyAla 63
Db 171 TTTCAGTCGATACCGTCATATGTCACATGCAAGTGCACATCTTCTTCTTACTACGCA 230
QY 64 TyrcLeuArgLysAAsnAlaTyrcLeu1leValSer1leAsnGlyPheGlyCyValAla1leGlu 83
Db 231 ATCTAGTAAGACACATGCTATCTATCATCTTATGATTAATTAACACCTTTGAGTGTTCATGAA 290

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QY 84 LeuThrTyrlSerLeuPheLeuPheTyTyAlaProArgLysSerLys1lePheThrgLys 103
Db 291 ATCTCCACTTGTTCCTATATCTTATGACCAAGAGAGATATCCACGTTG 350
QY 104 TrpLeuMetLeuLeu---GluLeuGlyAlaLeuGlyMetValMetPro1leThrTyLeu 122
Db 351 AAGTTGATGATGATAGCAACACCGGTCGACCGTTGATGAGGTTTGCTGCTCAAGCTC 410
QY 123 LeuAlaGluGlySerHisArgValMetLeValGlyTrp1leCyValAla1leAsnVal 142
Db 411 TTGGTTCCAAACAAACACCGCGTCGACCGTTGATGAGGTTTGCTGCTCAAGCTC 470
QY 143 AlValPheAlaAlaProLeuSer1leMetArgGlnVal1leTyThrLysSerValGlu 162
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QY 163 PheMetProPheThrLeuSerLeuPheLeuThrLeuCyValAlaThrMetTrpPhePheTy 182
Db 531 TACATGCCGTTTCTTCTCTCTGCTCTCACTTAAACCGCGTCATGTCGTCCTTTAT 590
QY 183 GlyPhePheLysAspPheTyTyAlaPheProAsn1leLeuGlyPheLeuPheGly 202
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QY 203 IleValGlnMetLeuLeuTyTyPheValTyTyLysAspSerLysArg1leAspAspGluLys 222
Db 651 GTAGCTCAGATGATACATATCATGATGATATCAAGGTTCCACGAAACGATTTGCCAACA 710
QY 223 SerAspProValArgGluAlaThrLysSerLysGluGlyValGlu1leIleAsn1le 242
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RESULT 7
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AC AB213458;
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DT 21-JAN-2003 (first entry)
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DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1263.
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KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN W0200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001MO-US026685.
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PR 26-JAN-2001; 2001US-0264647P.
XX
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PA (SYGN ) SYNSENTA PARTICIPATIONS AG.
XX
PI Harper JF, Krebs J, Wang X, Zhu T;
XX
WP1; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 15; SEQ ID NO 1263; 577bp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant

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 Query Match: 46.08%
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US-09-743-885A-1 (1-265) x AAC33408 (1-1263)


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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 2,89e-60 Length: 1177
Score: 622.00 Matches: 126
Percent Similarity: 65.40% Conservative: 46
Best Local Similarity: 47.91% Mismatches: 63
Query Match: 45.97% Indels: 28
DB: 3 Gaps: 4

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QY 70 TyrlleuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrlIleSerIle 89
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XX
DT 17-OCT-2000 (first entry)
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KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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US-09-743-885a-1 (1-265) x AAC49937 (1-1219)

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PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160815P.

[illegible]

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 24, 2004, 21:04:27 ; Search time 5448 Seconds
(without alignments)
2300.252 Million cell updates/sec

Title: US-09-743-885A-1
Perfect score: 1353
Sequence: 1 MAQLRDDSLFGLGNTV.....NSDNALQSMKXPSRLRTSK 265

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlp
-Q/cgnt.1/USPTO.spool.p/US09743885/runat.23122004.165258.9632/app.query.fasta.1.455
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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45
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-OUTFMT=pcr -NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
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8: gb_pl.*
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11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1353	100.0	1182	8 AF313914	Petunia x hybrida
2	1353	100.0	1205	6 BD217625	Method of
3	1353	100.0	1205	6 AX06355	Sequence
4	703.5	52.0	902	8 AY086047	Arabidops

5	656	48.5	1117	8 MTN3	Y08726 M.truncatui
6	652	48.2	1428	8 BT013320	BT013320 Lycopersi
7	647	47.8	1562	8 AK103266	AK103266 Oryza sat
8	646.5	47.8	1494	8 AK101913	AK101913 Oryza sat
9	623.5	46.1	879	6 AX506568	AX506568 Sequence
10	623.5	46.1	910	8 AY113934	AY113934 Arabidops
11	623.5	46.1	1269	8 AY087836	AY087836 Arabidops
12	623.5	46.1	1291	8 AY045949	AY045949 Arabidops
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15	622	46.0	901	8 AY096594	AY096594 Arabidops
16	622	46.0	1157	8 AF361825	AF361825 Arabidops
17	622	46.0	1172	8 AF419559	AF419559 Arabidops
18	622	46.0	1176	8 BT000808	BT000808 Arabidops
19	622	46.0	1196	8 AY070412	AY070412 Arabidops
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24	618	45.7	1124	8 AY116672	AY116672 Arabidops
25	618	45.7	1209	8 AP095641	AP095641 Arabidops
26	618	45.7	1279	8 AY057575	AY057575 Arabidops
27	590	43.6	1252	8 AY087516	AY087516 Arabidops
28	571.5	42.2	1492	8 AK109114	AK109114 Oryza sat
29	539	39.8	1500	8 AK106127	AK106127 Oryza sat
30	535	39.5	1517	8 AK070510	AK070510 Oryza sat
31	535	39.5	128673	8 AP005299	AP005299 Oryza sat
32	523.5	38.7	96827	8 AC005770	AC005770 Arabidops
33	484	35.8	134938	2 AC137759	AC137759 Oryza sat
34	474.5	35.1	82207	8 AT119155	AT119155 Arabidops
35	467.5	34.6	66087	8 AB023037	AB023037 Arabidops
36	463.5	34.3	2667	8 MTB307887	MTB307887 Medicago
37	462.5	34.2	154826	8 CNGS07YP4	AL713927 Oryza sat
38	462	34.1	944	8 BT002983	BT002983 Arabidops
39	447	33.0	775	8 BT005476	BT005476 Arabidops
40	447	33.0	960	8 BT004185	BT004185 Arabidops
41	447	33.0	990	8 AY088391	AY088391 Arabidops
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43	440.5	32.6	1208	8 AK067960	AK067960 Oryza sat
44	435.5	32.2	693	8 BT010528	BT010528 Arabidops
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	
AF313914	AF313914	Petunia x hybrida NECL mRNA, complete cds.	AF313914	AF313914.1	GI:11345412	Petunia x hybrida	Petunia x hybrida	1	(bases 1 to 1182)	Ge,Y.-X., Angenent,G.C., Wittlich,P.E., Peter,J., Franken,J., and Buescher,M., Zhang,L.-M., Dahlhaus,E., Kater,M.M., Willems,G.J. and Creemers-Molenaar,T.	Creemers-Molenaar,T.	2	(bases 1 to 1182)	Ge,Y.-X., Angenent,G.C., Dahlhaus,E., Franken,J., Willems,G.J. and Creemers-Molenaar,T.	Partial gene silencing of NECL results in early opening of anthers in Petunia hybrida	Mol. Gen. Genet. (2001) In press	3	(bases 1 to 1182)
AF313914	AF313914	Petunia x hybrida NECL mRNA, complete cds.	AF313914	AF313914.1	GI:11345412	Petunia x hybrida	Petunia x hybrida	1	(bases 1 to 1182)	Ge,Y.-X., Angenent,G.C., Wittlich,P.E., Peter,J., Franken,J., and Buescher,M., Zhang,L.-M., Dahlhaus,E., Kater,M.M., Willems,G.J. and Creemers-Molenaar,T.	Creemers-Molenaar,T.	2	(bases 1 to 1182)	Ge,Y.-X., Angenent,G.C., Dahlhaus,E., Franken,J., Willems,G.J. and Creemers-Molenaar,T.	Partial gene silencing of NECL results in early opening of anthers in Petunia hybrida	Mol. Gen. Genet. (2001) In press	3	(bases 1 to 1182)

AUTHORS Creemers-Molenaar,T., Ge,Y.-X. and Angenent,G.C.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2000) Plant Development and Reproduction, Plant Research International, Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands

FEATURES

source

Location/Qualifiers

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56..853

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ORIGIN

Alignment Scores:

Pred. No.: 5.95e-116 Length: 1182
Score: 1353.00 Matches: 265
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-743-885A-1 (1-265) x AF313914 (1-1182)

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Db 116 TCATTACGTGCTTCCTAGACCCGTCGCAACATTTTACAAATATATATAAAGAAATCA 175
QY 41 SerGlnGlyTyrglnAlaIleProTyMetValAlaLeuPheSerAlaGlyLeuLeuLeu 60
Db 176 TCAGAGGATATACAGCAAT 235
QY 61 TyrlYsAlaTyrlYsLeuAArgLysAAsnAlaTyrlYsLeuIleValSerIleAAsnGlyPheGlyCys 80
Db 236 TATTATGCTTATCTCAGGAAGAAATGCCATCTTATCGACGATTAATGCTTTGGATGT 295
QY 81 AlaIleGlnLeuThrTyrlYsSerLeuPheLeuPheTyrlYsAlaProArgLysSerLysIle 100
Db 296 GCCATTGAAATTAACATATATCTCTCTGTTTCTCTTTTACGGCCGACGAAAGCTTAAGATT 355
QY 101 PheThrgIyTrPleuMetLeuLeuGlnLeuGlyAlaLeuGlyMetValMetProIleThr 120
Db 356 TTTCAGAGGTGCGATGCTCTTGAATATGGAGCCCTCAGAAATGGATGATCCCAATTACT 415
QY 121 TyrlYsLeuAlaGlyLysSerHisArgValMetIleValGlyTyrlYsCysAlaAlaIle 140
Db 416 TATTATTAGCAAGAGGCTCATAGACTGATGATAGTGGATGGATTGGCGAGCTATC 475
QY 141 AAsnValAlaValPheAlaAlaProLeuSerIleMetArgGlnValIleLysThrLysSer 160
Db 476 AATGTGCTGCTTGTGCTGCTCTTTAAGCATCATGAGGCAAGTAATATAAACAAGAGT 535
QY 161 ValGlnPheMetProPheThrLeuSerLeuPheLeuThrLeuCysAlaIleMetTrpPhe 180
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QY 181 PheTyrgIyPhePheLysLysAspPheTyrlYsIleAlaPheProAsnIleLeuGlyPheLeu 200
Db 596 TTCTATGGGTTTTCAGAGAGGACTTTTACATTCGCTTTCCAAATATATCTGGGCTTTCTTA 655

QY 201 PheGlyIleValGlnMetLeuLeuTyrlYsValTyrlYsAspSerLysArgIleAspAsp 220
Db 656 TTGGGAATCGTTCAATAGCTATATATATTTGTTTACAAAGGATTCAAAGAAATAGATATC 715
QY 221 GlnLysSerAspProValArgGlnAlaThrlYsSerLysGlnGlyValGlnIleIle 240
Db 716 GAAATAATCTATCTGTCGAGAGGCTACAAATATCAAAAGAGGTGAGAAATCATATATC 775
QY 241 AsnIleGlnAspAspAsnSerAspAsnAlaLeuGlnSerMetGlnLysAspPheSerArg 260
Db 776 AACATTGAATGATATATTTGATTAACGATTCGACATTCAGAGAGAGATTTTCCAGA 835
QY 261 LeuArgThrSerLys 265
Db 836 CTCGCGGACATCAAAA 850

RESULT 2

BD217625 1205 bp DNA linear PAT 17-JUL-2003

LOCUS Method of collecting metabolite from modified nectar by insect.

DEFINITION

BD217625

BD217625.1 GI:33027395

ACCESSION

BD217625

KEYWORDS

JP 2002520064-A/1.

SOURCE

Petunia x hybrida

ORGANISM

Petunia x hybrida

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Petunia.
1 (bases 1 to 1205)
Creemers,J., Angenent,G.C. and Kater,M.M.
Method of collecting metabolite from modified nectar by insect
Patent: JP 2002520064-A 1 09-JUL-2002;
STITCHING CENTRUM VOOR PLANTENVERBEDINGEN EN REPRODUKTIEONDERZOEK
OS Petunia x hybrida
PN JP 2002520064-A/1
PD 09-JUL-2002 JP 2000560273
PF 15-JUL-1999 JP 2000560273
PR 16-JUL-1998 EP 98202375.6,14-DEC-1998 EP 98204215.2 PI
JANTINA CREEMERS,GERRIT CORNELIS ANGENENT,MARTIN MARIA KATER PC
C12N15/09,A01H5/00,A23L1/08,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
10,C12N5/10//
PC C07K14/415,C12N15/00,C12N5/00,C12N5/00
CC strain: W115
CC tissue type: nectar gland
CC NEC1
FH Key
FT CDS Location/Qualifiers

FEATURES

source

1..1205 Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

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Score: 1353.00 Matches: 265
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-743-885A-1 (1-265) x BD217625 (1-1205)

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Db 139 TCATTACGTGCTTCCTAGACACCGTCGCAACATTTTACAAATATATATAAAGAAATCA 198
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QY	21	SerPheMetValPheLeuAlaProValProThrPheTyrlsIleTyrlsArgIysSer	40
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QY	41	SerGluGlyTyrglnAlaIleProTyrlMetValAlaLeuPheSerAlaGlyLeuLeuLeu	60
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Db	439	TATTTATTATGACAGAGGCTCATCATAAGGTATGATGTGGATGATTGTGCAGCTATC	498
QY	141	AaMValAlaValPheAlaAlaProLeuSerIleMetTyrglnValIleIleTyrlsSer	160
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DEFINITION	Arabidopsis thaliana clone 20810 mRNA, complete sequence.		
VERSION	AY086047.1	GI:21404757	
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	1 (bases 1 to 902) Haas, J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.		
TITLE	Full-length messenger RNA sequences greatly improve genome annotation		
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)		
MEDLINE	22088475		
PUBMED	12093376		
REFERENCE	2 (bases 1 to 902)		
AUTHORS	Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.		
TITLE	Unpublished		
JOURNAL	Full-length cDNA from Arabidopsis thaliana		
REFERENCE	3 (bases 1 to 902)		
AUTHORS	Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA		
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.		
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ORIGIN			
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Fred. No.:	703.50	Matches:	136
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Percent Similarity:			

Best Local Similarity:	55.06%	Mismatches:	62
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DB:	8	Gaps:	1
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Qy	24	ValPheLeuAlaPProValPProThThPheThyTylsIleTylsArgLysSerSerGluGly	43
Db	111	GTGTTCTTTGTACACCAAGTCCCAAGCTTTTATGGAGATATACAAAGAAATATCAAAAGG	170
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Db	171	TTTCAGTGCATACCGTACATATATGACATAGCAAGTCAACTCTTCTCTACTACGGA	230
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Db	231	ATCATAGAAAGACACATGCTTATCTGATCTATGATATTAACACTTGGATGTTTCATTTGA	290
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Qy	104	TriPheMetLeuLeu--GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeu	122
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Qy	163	PheMetProPheThrLeuSerLeuPheLeuThrLeuCysAlaAlaMetTyrPhePheTyr	182
Db	531	TACATGCGGTTCTTCT	590
Qy	183	GlyPhePheLysLysAspPheTyrIleAlaPheProAaenIleLeuGlyPheLeuPheGly	202
Db	591	GGACTTCTTATCAAAAGCAAGTCAATGCTATGCAAAATCTTCGTTTCTTATTCGCT	650
Qy	203	IleValGlnMetLeuLeuTyrPheValTyrTyrLysAspSerLysArgIleAspAspGluLys	222
Db	651	GTACTCTAGATGATATCTATATACATATATCAAGGTTACACAAAGATTTGCCAACAA	710
Qy	223	SerAspProValArgGluAlaThyLysSerLysGluGlyValGluIleIleAaenIle	242
Db	711	GAGAACCAACATAGCAAAATMAAACCGATTTAAACAAAGTCCCGATCGTGGCCTTGAATTG	770
Qy	243	GluAspAspAspAspSerAspAsp 249	
Db	771	CCTGATGTCGATCAGACAAAT 791	
RESULT 5			
MTN3	MTN3	1117 bp	linear
LOCUS	M.truncatula mRNA for MTN3 gene.		
DEFINITION	Y08726		
ACCESSION	Y08726.1 GI:1619601		
VERSION			
KEYWORDS	MTN3 gene.		
SOURCE	Medicago truncatula (barrel medic)		
ORGANISM	Medicago truncatula		
REFERENCE	1 (bases 1 to 1117)		
AUTHORS	Gamas,P., Niebel Pde,C., Lescure,N. and Cullimore,J.		

TITLE	Use of a subtractive hybridization approach to identify new					
JOURNAL	Medicago truncatula genes induced during root nodule development					
MEDLINE	Mo. Plant Microbe Interact. 9 (4), 233-242 (1996)					
PUBMED	8634476					
REFERENCE	2 (bases 1 to 117)					
AUTHORS	Gamas, P.					
TITLE	Direct Submission					
JOURNAL	Submitted (08-OCT-1996) P. Gamas, CNRS-INRA, LBMRM, Chemin De					
	Borde Rouge BP27, Castanet-Tolosan Cedex, 31326, FRANCE					
FEATURES	Location/Qualifiers					
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	/gene="MtN3"					
	115..921					
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	VEHPFNLSFTLTSTATMPGVGFELDKICXLPNVLGXVIGLIOMLIXAYIRNGEGR					
	AMKEKKRAPLEPPKSIVLETQLERIKBOEKAKDDNEBKDSSEPTGGV"					
sig_peptide	115..204					
	/gene="MtN3"					
	/note="putative"					
Alignment Scores:						
Pred. No.:	1.69e-51	Length:	1117			
Score:	656.00	Matches:	129			
Percent Similarity:	68.80%	Conservative:	54			
Best Local Similarity:	48.50%	Mismatches:	55			
Query Match:	48.48%	Indels:	28			
Difference:	8	Gaps:	6			
US-09-743-885A-1 (1-265) x MTN3 (1-117)						
Qy	9	LeuSerPheIlePheGlyLeuLeuGlyValAsnIleValSerPheMetValPheLeuAlaPro	28			
Dd	136	TTGGCTTTCACCTTTGGCATCGTGGAATCAATTCGTCTTGATTCCTGGCTCCA	195			
Qy	29	ValProThrPheTyrlsyleIleTyrlsyrAsgllysSerSergIugLyTYrGlAlalalePro	48			
Dd	196	ATAACAACATTTCAGCATTATACAGAAGAAATGACAGAGGGTTTCAAGTCACTACT	255			
Qy	49	TyrMetValAlaLeuPheSerAlaGlyLeuLeuLeuTyTYrAlaTYrLeuAlaGlyAsn	68			
Dd	256	TACCAAGTAGCTTGTTCAGCTCCATGCTGTTGGTGTACTATGCATTCCTCAAAAAAAGAT	315			
Qy	69	AlaTYrLeuIleValSerIleasnGlyPheGlyCyAlaalleGlyLeuThTYrIleser	88			
Dd	316	GCTTTTCCCACATTACATTAACATCATTTGGATGTGTGTAGAGACCATCTACATCATTA	375			
Qy	89	LeuPheLeuPheTYrAlaProArglysSerIysIlePheThrGlyTYrPheuMet---Leu	107			
Dd	376	TTTGACATCATCTATGACCAAGGAGATGCCAAGAACTTAACCTTTCAAGTACTTTCGGCA	435			
Qy	108	LeuGluLeuGlyAlaLeuGlyMetValMetProIleThTYrLeuLeuAlaGluGlySer	127			
Dd	436	ATGAATGGGGGTCTTGGCTTGAATCTCTCAATGACCTAATCTAGCCGTGATGATGCA	495			
Qy	128	HiearGValMetIleValGlyTYrPileCyAlaAlaIleasnValAlaValPheAlaAla	147			

Dd		496	CTTGGTGTCACCAAGTTCTCGATGGGTTTTGTGTCCCTTACTGTAAGTNTTTGCACA	555
Oy		148	ProLeuseriIleCtaArgInValIIleLysThrLysSerValGIuPheMetProPheThr	167
Dd		556	CCACTAAGCATGTGGCTCAAGTTGTTCTGTCAAGAAGGTGTGAATTATATCCTTTCAAT	615
Oy		168	LeuSeriLeuPheLeuThrLeuCysAlaIThMetTrpPhePheTYrGIuYpHePhenyllys	187
Dd		616	TTCGATTTCACTCTCACACATTGAGTGCACCAATGTGGTTGGNTATGGTTTTTCTCTCAG	675
Oy		188	AspPheTYrIIeAlaPheProAsnIIleuGIuYpHeLeuPheGIuIleValIGlmetLeu	207
Dd		676	GACATATGCATGTTATTTAACCAAATGCTGTGGTTTNGATTTGGGGTTACTCAATGCTA	735
Oy		208	LeuTYrPheValTYrLYASA-----SerLYARgIIeaPaapGIuLYSerAspPro	225
Dd		736	CTGATATCAATTTTACAGAAATGCTGGGAAAAACCTATGAAAAGAAAGAAAGACCA	795
Oy		226	ValArgGIuAlaThrLYSerSerLYGluGIuValGIuIleIlelle-----	240
Dd		796	ATT---GAGCCACCACCAAAAGT-----ATTGTTATAGAGCCCAATTGGAG	837
Oy		241	-----AsnIIeGIuAspaAspaSenSerAspaAsnaIIeUglInsEr	253
Dd		838	AAATTTGAACACAGAAAAAGACAAACAGATGATATATAATGAG-----	879
Oy		254	MetGIuLYAspPheSer	259
Dd		880	---GAAAAAGTAAAGT	894
RESULT 6				
BT013320				
LOCUS	BT013320	1428 bp	mRNA	linear PLN 11-MAY-2004
DEFINITION	Lycopersicon esculentum clone 13501OF, mRNA sequence.			
ACCESSION	BT013320			
VERSION	BT013320.1 GI:47104735			
KEYWORDS	FLI_CDNA.			
SOURCE	Lycopersicon esculentum (tomato)			
ORGANISM	Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.			
REFERENCE	1 (bases 1 to 1428) Kirtnes, B.F., Wang, W. and Vazeille, A.			
AUTHORS	Direct Submission			
TITLE	Submitted (11-MAY-2004) The Institute for Genomic Research, 9712			
JOURNAL	Medical Center Drive, Rockville, MD 20850, USA			
FEATURES				
Source	Location/Qualifiers			
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ORIGIN				
Alignment Scores:				
Pred. No.:	5 29e-51	Length:	1428	
Score:	652.00	Matches:	128	
Percent Similarity:	70.40%	Conservative:	48	
Best Local Similarity:	51.20%	Mismatch:	66	
Query Match:	48.19%	Indels:	8	
DB:	8	Gaps:	3	
US-09-743-885A-1 (1-265) x BT013320 (1-1428)				
Oy		10	serPheIlePheGIuLeuGIuYAasnIIeValSerPheMetValPheLeuAlaProVal	29
Dd		193	GCTTTTGCTTTGGTGTGTCCTTGGTAACATTAATCTCGTTACATGTGTTCTTCCACATA	252
Oy		30	ProthrPheTYrLYSAIIeTYrLYSARGLYSereSeRGLuGYrYGlnAlaIIleProTYr	49

Db	Accession	LOCUS	DEFINITION	ORIGIN	REFERENCE
Db	253	CCCAAGTTCATAGCATTTACAGAAGAAATCAACAGAAGGTATCATCATTCATTC	312		
Qy	50	MctVal1AlaLeuPheSerAlaGlyLeuLeuLeuTyrTyrAlaTyrLeuArgLysAsnAla	69		
Db	313	GTGGTGGCGCTTACTAGTTCATGCTGGATATATATATGACCTTTGGAATCCAAACATG	372		
Qy	70	TyrLeuIleValSerIleAsnGlyPheGlyCysAlaIleGluLeuThrTyrIleSerLeu	89		
Db	373	CCCCCTACTCATTCACATTAACCTCCCTTGGATATGTTTCATTGAGACTATCATCGTGGTTTC	432		
Qy	90	PheLeuPheTyrAlaProArgLysSerLysIlePheThr---GlyTyrLeuMetLeuLeu	108		
Db	433	TACCTTTTCTACGACCCAAAGAAAGCCAGGCGCATCTATATAAATGCTCATGTATCA	492		
Qy	109	GluLeuGlyAlaLeuGlyMetValMetProIleThrTyrLeuLeuAlaGluLysSerHis	128		
Db	493	GTGGTGGTGGATTTGGTGCATATAGTGTAGTACTGAAATTTCTATTCAAAGAGTCTGTT	552		
Qy	129	ArgValMetIleValGlyTyrIleGlyValAlaAlaIleAsnValAlaValPheAlaPro	148		
Db	553	CGTGGACAAATGTTGGATGGATGGATTTGCTTATTTTCTCTGTTGGTATTTGGTCTCC	612		
Qy	149	LeuSerIleMetArgGlnValIleLysThrLysSerValGluPheMetProPheThrLeu	168		
Db	613	TTAGGCGATTTGGAGACACAGATCATCAAGACCAAGATGTGGATATACATGCCATCTCTCTTA	672		
Qy	169	SerLeuPheLeuThrLeuCysAlaThrMetTyrPhePheTyrGlyPhePheLysLysAsp	188		
Db	673	TCAGTATTTCACATTTAAGTCTGTATGTCGTTCTTCTATAGTCTTCTACTATAAGAT	732		
Qy	189	PheTyrIleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGluMetLeuLeu	208		
Db	733	ATTACATATGTCCTCCAAATGTTTGGGGTTCACCTTGGATATCTCCAAATTTTACTC	792		
Qy	209	TyrPheValTyr---LysAspSerLysArgIleAspAspGluLysSerAspProValArg	227		
Db	793	TATGCAATATTCAGCAAAAAGAGAAATGCCATCAATAAGAACAGAACTTCCAGAGATA	852		
Qy	228	GluAlaThrLysSerLysGluGlyValGluIleIleIleAsnIleGluAspAspAsnSer	247		
Db	853	CAAAAGACT-----GAGCAATTTGGGAAGATGAGAACTGATGATGA	894		
Qy	248	AspAsnAlaLeuGlnSerMetGluLysAsp	257		
Db	895	AATAAGAGCTTCCAGAACTCACACAAAGAA	924		
RESULT 7					
AKI03266					
LOCUS	AKI03266	1562 bp	mRNA	linear	PLN 24-UTL-2007
DEFINITION	Oryza sativa (japonica cultivar-group)	cdna clone:J03124G19, full			
ACCESSION	AKI03266				
VERSION	AKI03266.1	GI:32988475			
KEYWORDS	FLU_CDNA, CAP trapper.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	1				
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of				
	Agronomical Sciences Rice Full-Length cDNA Project Team;				
	Kiuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,				
	Kishimoto,N., Yazaraki,J., Ishikawa,M., Yamada,H., Ooka,H.,				
	Ohtsuka,K., Nemiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,				
	Onishi,K., Shieniki,T., Foundation of Advancement of International				
	Science Genome Sequencing & Analysis Group;; Tsunoda,Y.,				
	Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Okumoto,Y.,				
	Kurosaki,T., Kodama,T., Maeda,H., Kobayashi,M., Xie,Q., Lu,M.,				
	Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishida,J.,				
	Ikedo,R., Ishibiki,Y., Kawamata,M., Yoshimura,A., Miura,U.,				
	Kusunugi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;				
	Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.				

TITLE	JOURNAL	REFERENCE	AUTHORS
<p>2 (bases 1 to 1562)</p> <p>12869764</p> <p>22752273</p>	<p>ADACHI, T., AIZAWA, K., AKIMURA, T., ARAKAWA, T., CERNINCI, P., DOI, K., FUJIMURA, T., FUKUDA, S., HANAGAKI, T., HARA, A., HASHIZUME, W., HAYASHIDA, K., HAYASHIZAKI, Y., HAYATSU, N., HIRAMOTO, K., HIROKA, T., HORI, F., HOTTA, I., IIDA, J., IIDA, Y., IKEDA, R., IIMURA, K., IMOTANI, K., ISHIBIKI, J., ISHII, Y., ISHIKAWA, M., ITOH, M., KAGAWA, I., KANAGAWA, S., KATOH, H., KAWAGASHIRA, N., KAWAI, J., KAWAMATA, M., KIKUCHI, S., KISHIKAWA-HIROZANE, T., KISHIMOTO, N., KOBAYASHI, M., KODA, S., KOJIMA, K., KOJIMA, Y., KONDO, S., KONNO, H., KOUNDA, M., KOSADA, S., KUTIHARA, C., KUROSAKI, T., KUSUNEGI, T., LI, C., LU, M., MASUDA, H., MATSUBARA, K., MATSUYAMA, T., MIRA, J., MIYAZAKI, A., MIZUNO, K., MURAKAMI, K., MURAKA, M., NAGATA, T., NAMURA, M., NAMIKI, T., NARIKAWA, K., NIKURA, J., NISHI, K., NOMURA, K., NUMASAKI, R., OHNEDA, E., OHNO, Y., OHNO, M., OHTSUKI, K., OKA, M., OKURA, H., OSAO, T., OSAI, Y., OTSU, Y., RYU, R., SATOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N., SANO, H., SASEKI, D., SATO, K., SATOH, K., SHIBATA, K., SHINGAWA, A., SHIRAKI, T., SHISHIKI, T., SOGABE, Y., SUGANO, S., SUGIYAMA, A., SUZUKI, K., SUZUKI, Y., TAGAMI, M., TAGAMI-TAKEDA, Y., TAGAWA, A., TAKAHASHI, F., TAKAKU-AKASHI, S., TANAKA, T., TOMARU, A., TOYA, T., TSUNODA, Y., UEDA, M., WAKI, K., XIE, Q., YAHAGI, W., YAMADA, H., YAMAMOTO, M., YASUNISHI, A., YAZAKI, J., YOKOMIZO, S. and YOSHIMURA, A.</p>	<p>Direct Submission</p> <p>Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tenkuba, Ibaraki 305-8602 Japan (E-mail: ekikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)</p> <p>This clone is one of the 28K full-length cDNA clones from japonica rice.</p>	<p>URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S.,Satoh_K.,Nagata_T.,Kawagashira_N.,Doi_K.,Kishimoto_N.,Yazaki_J.,Ishikawa_M.,Yamada_H.,Ooka_H.,Hotta_I.,Kojima_K.,Namiki_T.,Ohneda_E.,Yahagi_W.,Suzuki_K.,Li_C.,Ohtsuki_K.,Shishiki_T.and_Yamamoto_M.</p> <p>FAIS Genome Sequencing & Analysis Group: Otsuno, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotsaki, T., Kusunegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., SugiYama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.</p> <p>Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken</p> <p>Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Cerninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hiroyaka, T., Hori, F., Iida, J., Iimura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kishikawa-Hirozane, T., Kojima, Y., Kojima, Y., Kondo, S., Kouda, M., Koya, S., Kutihara, C., Matsuyama, T., Miyazaki, A., Murata, M., NakaYama, M., Nishi, K., Nomura, K., Numasaki, R., Onno, M., Otsuo, N., Osa, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashi, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.</p>

Alignment Scores:

Pred. No.:	1,7e-50	Length:	1562
Score:	647.00	Matches:	116
Percent Similarity:	73.48%	Conservative:	53
Best Local Similarity:	50.43%	Mismatches:	55
Query Match:	47.82%	Indels:	6
		Gaps:	2

US-09-743-885a-1 (1-265) x AK103266 (1-1562)

```

Qy 10 SerPheIlePheLeuGlyLeuGlyValSerPheMetValPheLeuAlaProVal 29
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Db 411 GACCTGCTGCTACCATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 470
Qy 90 PheLeuPheTyrAlaProAlaGlySerIlePheThrGlyTyrIleuMetLeu---Leu 108
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 471 TACCTGCGCTACCGCCCAAGACGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530
Qy 109 GlnLeuGlyValAlaLeuGlyMetValMetProIleThrTyrIleuLeuAlaGlySerHis 128
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Db 531 AACATGCGCTCTTGGCGGTATCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
Qy 129 ArgValMetIleValGlyTyrIleCysAlaAlaIleAsnValAlaValPheAlaAlaPro 148
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Db 591 CGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
Qy 149 LeuSerIleMetArgGlnValIleLeuThrIleSerValGlnPheMetProPheThrLeu 168
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Db 651 TTGAGCATCATCAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
Qy 169 SerLeuPheLeuThrLeuGlyAlaThrMetTyrPhePheTyrGlyPhePheLeuValAsp 188
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Db 711 TCTCTTCTTCTGCTGCTTACCGCGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 770
Qy 189 PheTyrIleAlaPheProAlaIleLeuGlyPheLeuPheGlyIleValGlnMetLeuLeu 208
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Db 771 GTGTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
Qy 209 TyrPheValTyrIleAspSerIleValArgIleAspAlaIleValSerAspProValArgGln 228
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Db 831 TACATGCGCGTACCGAAGACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890
Qy 229 AlaThrIleSerIleGlyValGlnIle 238
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Db 891 GCC-----GGGCTGAGATC 905

```

RESULT 8
AK101913
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J033071H09, full insert sequence.
ACCESSION
AK101913
VERSION
AK101913.1 GI:32987122
KEYWORDS
FLI CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1

AUTHORS

The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, S., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ohtomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikiura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Heshidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oota, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

2 (bases 1 to 1494)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Heshizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imanura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikiura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oota, N., Ota, Y., Ohtomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashi, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica rice.
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Ohtomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Heshizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imanura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, N.,

COMMENT

Db	Accession	Version	KeyWords	Organism	Reference	Title	Journal	Authors
Db	568	AATGACATATGATGATGCGATTCGCAACGTCGTGGGATTCGTACTGATGGGCTGTGGAANTG	627					
Qy	207	LeuLeuTyrPheValTyrTyrLeuSerLysArg	217					
Db	628	GTGTTGTACTGCTGTTACAGGAACCTCAATGAAACACAGAGAGATTAAATTCGTGAGNA	687					
Qy	218	-----1le 218						
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Qy	219	AspAspGluTyrSerAspPheValArgGluValThrLysSerLysGluCysValGluIle	238					
Db	748	GTGACGGAATCGGTGCACCACTCTCTGAGCCGTT-----CATCATGAGGATCTGTCCAA	804					
Qy	239	IleIleAsnIleGluAspAspAsnSerAspAsn	249					
Db	805	GTACTTAAGATGAGAGAGCCCTCATATTGAAAC	837					
RESULT 10								
Accession	AY113934	910 bp	mRNA	linear	PLN 18-SEP-2002			
Definition	Arabidopsis thaliana putative senescence-associated protein SAG29 (AtSG13170)	mRNA, complete cds.						
Version	AY113934							
KeyWords	AY113934.1	GI:21281009						
Source	FLI CDNA.							
Organism	Arabidopsis thaliana (chale cress)							
Reference	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.							
Authors	Yanada, K., Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldemith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Tortum, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamuya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Saeou, M., Seki, M., Shim, P., Southwick, A., Shinzaki, K., Davis, R. W., Ecker, J. R. and Theologis, A.							
Title	Arabidopsis Open Reading Frame (ORF) Clones							
Journal	Unpublished							
Reference	2 (bases 1 to 910)							
Authors	Yanada, K., Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldemith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Tortum, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamuya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Saeou, M., Seki, M., Shim, P., Southwick, A., Shinzaki, K., Davis, R. W., Ecker, J. R. and Theologis, A.							
Title	Direct Submission							
Journal	Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA							
Comment	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : RIKEN Arabidopsis Full-length cDNA) : Seki, M., Narusaka, M., Ishida, J., Saeou, M., Kamuya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.							
	The Salik, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yanada, K., Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldemith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Tortum, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C. J., Shim, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.							
	Yanada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed and to this work. Shinzaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.							

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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 TKSVEIMPTLSFPLTISAVMPPAYGFLNDICITAINVGVFLGLQMTLYLVYRNS
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ORIGIN
 3'UTR

Alignment Scores:
 Pred. No.: 1,35e-48 Length: 910
 Score: 623.50 Matches: 119
 Percent Similarity: 65.31% Conservative: 58
 Best Local Similarity: 43.91% Mismatches: 63
 Query Match: 46.08% Indels: 31
 Db: 8 Gaps: 4

US-09-743-085A-1 (1-265) x AY113934 (1-910)

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Oy      29  ValProthPheTy1y1e1eTy1y1eAry1y1eSerSerG1y1y1y1y1y1y1y1lePro 48
Db      88  GTGGCAACTTTTATAGAAATATACAGAGAAATACGAGAAAGTTTCCAGTCGCTACCG 147

Oy      49  TyMetValAlaLeuPheSerAlaG1yLeuLeuLeuTy1y1y1AlaTy1y1eAry1y1eAaen 68
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Oy      69  AlaTy1y1eLeu1eValSer1eAeG1yPheG1yCy1y1Ala1eG1yLeuThTy1y1leSer 88
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Oy      108  LeuG1yLeuG1yAlaLeuG1yMetValMePro1eThTy1y1eLeuA1y1eG1ySer 127
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Oy      128  His---ArgValMet1eValG1yTy1y1eCy1y1AlaAla1eAaenValAlaValPheAla 146
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Oy      147  AlaProLeuSer11eMetAry1y1eVal11eLeuYerThry1y1eSerValG1yPheMetProPhe 166
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Qy      187 LysAspPheTyrlleAlaPheProAsnIleLeuGlyPheLeuPheGlyIleValGlnMet 206
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Qy      218 -----1le 218
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RESULT 11					
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LOCUS	AY087836	1269 bp	mRNA	linear	PLN 14-APR-2003
DEFINITION	Arabidopsis thaliana clone 38843 mRNA, complete sequence.				
ACCESSION	AY087836				
VERSION	AY087836.1	GI:21406587			

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 126)
REFERENCE Haas, B.J., Volfovsky, N., Town, C.D., Tronkhan, M., Alexandrov, N.,
 Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L.
AUTHORS Full-length messenger RNA sequences greatly improve genome
 annotation
TITLE Genome Biol. 3 (6), RESEARCH0029 (2002)
JOURNAL

PUMED
 12093376
 2 (bases 1 to 1269)
 Brover, V., Trounhan, M., Lu, Y.-P., Flavell, R. and
 AUTHORS

TITLE Full-length cDNA from *Arabidopsis thaliana*
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1269)
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made

this set was done by comparison with known proteins: two percent are 3'-truncated, approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Iaer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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ORIGIN		
Alignment Scores:		
Pred. No.:	2e-48	Length: 1269
Score:	623.50	Matches: 119
Percent Similarity:	65.31%	Conservative: 58
Best Local Similarity:	43.91%	Mismatches: 63
Query Match:	46.08%	Indels: 31
DB:	8	Gaps: 4

ORIGIN					
Alignment Scores:					
Pred. No.:	2e-48	Length:	1269		
Score:	623.50	Matches:	119		
Percent Similarity:	65.31%	Conservative:	58		
Best Local Similarity:	43.91%	Mismatches:	63		
Query Match:	46.08%	Indels:	31		
DB:	8	Gaps:	4		
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QY	49	TyrMetValAlaLeuPheSerAlaGLyLeuLeuLeuTYrZLyAlTyRLseuArgLYAsn	68		
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QY	69	AlatyrLeuIIeValserIIeaSnGLYPheGLYCysAlaIIeGuLeuThrTYrLIseser	88		
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QY	207	LeuLeuTYrPheValTYrLYsApSerLYsArg-----	217		
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Qy	239 lletleantlegluapapapserapapen 249
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LOCUS	AY045949
DEFINITION	Arabidopsis thaliana putative senescence-associated protein SAG39
ACCESSION	AY045949
VERSION	AY045949.1
KEYWORDS	FLI CDNA.
SOURCE	Arabidopsis thaliana (chale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryote, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 1291)
REFERENCE	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
TITLE	Arabidopsis Full Length cDNA Clones
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 1291)
TITLE	Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyer, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Theologis, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
JOURNAL	Direct Submission
COMMENT	Submitted (10-JUN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	RKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
COMMENT	The Sak, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Theologis, A., Davis, R.W., Ecker, J.R. and Theologis, A.
COMMENT	Yamada, K. (SSP/PGSC) and Seki, M. (RKEN GSC) contributed equally to this work. Shinozaki, K. (RKEN GSC) and Theologis, A. (SSP/PGSC) contributed equally to this work as PIs.
COMMENT	Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
COMMENT	Location/Qualifiers
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COMMENT	/organism="Arabidopsis thaliana"
COMMENT	/mol_type="mRNA"
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TKSEVMPELTLSPLTISAWMMPAYGLNDICAIPIWVGFILOMTLYLYRRNS
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3' UTR
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1276
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/note="artifact within poly A tail"

ORIGIN

Alignment Scores:
Pred. No.:      2,04e-48      Length:      1291
Score:          623.50       Matches:      119
Percent Similarity: 65.31%   Conservative:  58
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Query Match:    46.08%     Indels:       31
DB:             8          Gaps:         4

US-09-743-885A-1 (1-265) x AY045949 (1-1291)

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Db      344 GCTTTTCCTCAATTATTCATCACTCCCTTGGCGCGCGGAGACACTCTCATATAGCC 403
Oy      89 LeuPheLeuPheTyryrAlaProArgLyserIylePheThrIglTyrypleuMetLeu--- 107
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Oy      108 LeuGluleuEugIyalalaEugIyMetValMeProIleThyrTyryleuAlaIleGluIyser 127
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Oy      128 His---ArgValMetIleValIglTyriPleCySaAlaAlaIleAsnValAlaValPheaIa 146
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LOCUS			linear
DEFINITION	Sequence 1795 from Patent WO2004035798.		PAT 10-MAY-200
ACCESSION	CQ805384		
VERSION	CQ805384.1	GI:47111326	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
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	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE			
AUTHORS	Inze,D., de Veylder,L. and Vliethe,K.		
TITLE	Identification of novel e2f target genes and use thereof		
JOURNAL	Patent: WO 2004035798-A 1795 25-APR-2004;		
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Dd		271	TTCCTTGCCCTACGCCTCCCAAGCCAGCGCTCGGATGTGTACAAGAAGATGCTACTTATG	330
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Dd		451	CTAAGCATATATCAGACGAGTATAAACAAGAAGTGGAGTACATGCCCTTAGCTTA	510
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Dd		511	TCCTTAACCCCTTACCATCAGTGCCTGCTCATATGGCTCTTATGGTCTTGCTTCACAGAC	570
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Dd		571	ATCTATGTGTGTTCCCCGAATGTCTGTGTGTCTCTCGTGCATCTCCAATGATATCTC	630
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AY078041	DEFINITION	Arabidopsis thaliana AT3g48740/8p19_250 mRNA, complete cds.		
AY078041	VERSION	AY078041.1 GI:18700263		
KEYWORDS	SOURCE	Fli CDNA.		
ORGANISM		Arabidopsis thaliana (thale cress)		
REFERENCE		Arabidopsis thaliana		
AUTHORS		Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
		1 (bases 1 to 870)		
		Cheuk,R., Chen,H., Kim,C.-J., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayaashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.U., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Yamawake,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yanamure,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.		
		Arabidopsis cdna clones		
		Unpublished		
		2 (bases 1 to 870)		
		Cheuk,R., Chen,H., Kim,C.-J., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayaashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.U., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Yamawake,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yanamure,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.		
		Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K.,		

TITLE Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.
JOURNAL Direct Submission
Submitted (04-FEB-2002) Salk Institute Genomic Analysis Laboratory

COMMENT
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPD cDNAs (RAPD cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Natsuka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PECC (SSP) Consortium members carried out the sequencing and annotation of the RATL cDNAs: Cheuk, R., Chen, H., Kim, C.-U., Meyers, M.C., Shinn, P., Bahh, J., Bowser, L., Chan, M.M., Chang, E., Dale, J.-M., Deng, J.-M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.-M., Lin, J., Miranda, M., Nguyen, M., Onizuka, M.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriama, C., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Soti, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

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Pred. No.:	1.77e-48
Score:	622.00
Percent Similarity:	65.40%
Best Local Similarity:	47.91%
Query Match:	45.97%
DB:	8
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Qy	90	PheLeuPheTyrAlaProAlGlySerIleValIlePheThr---GIYrPlMetLeuLeu	108
Db	271	TTCTCTTGCCTACGCTCCCAAGCCAGCTCGGATGTGACAGGAAGATGCTACTTATG	330
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Db	811	ATTGAAGT	819

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VERSION	complete cds.
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AUTHORS	Arabidopsis thaliana
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	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsis.
	1 (bases 1 to 901)
	Yamada, K., Banth, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,

TITLE
JOURNAL
COMMENT

Shinozaki, K., Davis, R.W., Becker, J.R. and Theologis, A.
Direct Submission
Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN
Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
sequenced the PUN1 (ORF) clones using the RAPL cDNAs: Yamada, K.,
Bain, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.D., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
Southwick, A., Davis, R.W., Becker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to Genbank.

FEATURES

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Location/Qualifiers

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Query Match: 45.97% Indels: 28
DB: 8 Gaps: 4

US-09-743-885a-1 (1-265) x AY096594 (1-901)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2004, 19:39:56 ; Search time 135 Seconds
(without alignments)
1129.439 Million cell updates/sec

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Scoring table: BLOSUM62
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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41	350	25.9	202	2	Q9LPL1 Arabidopsis
42	325	24.0	238	2	Q9SN64 Arabidopsis
43	321.5	23.8	213	2	Q9FM10 Arabidopsis
44	319.5	23.6	249	2	Q8L628 Arabidopsis
45	313.5	23.2	263	2	Q9LRT5 Arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9FPN0	PRELIMINARY;	PRT;	265 AA.
AC	Q9FPN0			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	NEC1			
OS	Petunia hybrida (Petunia)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	lamiales; Solanales; Solanaceae; Petunia.			
OX	NCBI_TaxID=4102;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ge Y.-X., Angenent G.C., Dahlhaus E., Franken J., Willems G.J.,			
RA	Creemers-Molenaar T.;			
RT	"Partial gene silencing of NEC1 results in early opening of anthers in			
RT	Petunia hybrida.";			
RL	Mol. Gen. Genet. 0:0-0(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20575716; PubMed=1135107;			
RA	Ge Y.-X., Angenent G.C., Wittich P.E., Peter J., Franken J.,			
RA	Buscher M., Zhang L.-W., Dahlhaus E., Kater M.W., Willems G.J.,			
RA	Creemers-Molenaar T.;			
RT	"NEC1, a novel gene, highly expressed in nectary tissue of Petunia			
RT	hybrida.";			
RL	Plant J. 24:725-734(2000).			
DR	EMBL: AF13914; AAC34696.1; -.			
DR	GO: GO:0016020; C.membrane; IEA.			
DR	InterPro: IPR004316; MGN3_slv.			
DR	Pfam: PF03083; MGN3_slv; 2.			
DR	SEQUENCE 265 AA; 30256 MW; E6C6906B72A40C53 CRC64;			
Query Match	100.0%;	Score 1353;	DB 2;	Length 265;
Best Local Similarity	100.0%;	Pred. No. 7.9e-99;		
Matches 265;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAQLRADDSFIIFGLIGNIVSEFWFLAPVPTFYKIKRKSSEGYQAI	PPYVALFSAGLL	60
DB	1	MAQLRADDSFIIFGLIGNIVSEFWFLAPVPTFYKIKRKSSEGYQAI	PPYVALFSAGLL	60
QY	61	YVAVLRKNAVLYISNGFGCAITLTISLPLFAAPKSKITFTGMMLLBELGALGMNPT	120	
DB	61	YVAVLRKNAVLYISNGFGCAITLTISLPLFAAPKSKITFTGMMLLBELGALGMNPT	120	
QY	121	YLLAEGSHRMVITGICAIINVAFAAPISIMROVITKTSVEMPTLSLFTLCTATMP	180	
DB	121	YLLAEGSHRMVITGICAIINVAFAAPISIMROVITKTSVEMPTLSLFTLCTATMP	180	
QY	121	YLLAEGSHRMVITGICAIINVAFAAPISIMROVITKTSVEMPTLSLFTLCTATMP	180	
DB	121	YLLAEGSHRMVITGICAIINVAFAAPISIMROVITKTSVEMPTLSLFTLCTATMP	180	
QY	181	FYGFPPKDFYIAPNPITLGFGLIGVQMLLVFVYKDSKRIDKSDPYREATKSGEVEIII	240	
DB	181	FYGFPPKDFYIAPNPITLGFGLIGVQMLLVFVYKDSKRIDKSDPYREATKSGEVEIII	240	

QY	241	NIEDNSDNALOSMEKDFSRRLRTSK	265
Db	241	NIEDNSDNALOSMEKDFSRRLRTSK	265

RESULT 2			
ID	Q9ZV02	PRELIMINARY:	PRT: 258 AA.
AC	Q9ZV02:		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE	Similar to MCN3 protein.		
GN	Name=At2g39060;		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid 1; Brassicales; Brassicaceae; Arabidopsids.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,		
RA	Shen M., Romling C.M., Frazer C.M., Somerville C.R., Venter J.C.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Town C.D., Kaul S.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC005770; AAC79616.1; -.		
DR	PIR; F04812; F04812.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	InterPro; IPR004316; MCN3_slv.		
DR	Pfam; PF03083; MCN3_slv.2.		
SQ	SEQUENCE 258 AA; 28716 MW; 0C58F140C5864DBD CRC64;		

Query Match			
Best Local Similarity	52.1%;	Score 704.5;	DB 2; Length 258;
Matches 136;	Conservative 48;	Pred. No.1.2e-47;	Matches 62;
			Indels 1; Gaps 1
QY	4	LRADLSTIFGLGNIVSFPMFLAVPPFFKTKYRKSSSEGYALITYMALPSAGLLIYYA	63
Db	3	LKVEHIAELFGILGNIVSFGVFLSPVFFGYGKKSSKGFOSIPIYICALMSATLLIYYG	62
QY	64	YLRKAYIVISINGGCAILETVYISLFTFYAPRKSKITFGWIML-L-ELGALGMNPITYL	122
Db	63	IMKTHAYIISINTGCGFETISYLFYLYLAPREKAKITLKLIYCNIGGLILLVNL	122
QY	123	LAEGSHRWIVGWCALINAVFAAPLSIMROVITKTSVEFNPFTLSFLTLCAIMWFFY	182
Db	123	LVPKQHRVSTGVWCAYSLAVFASPLSVMRKVITKTSVEVNPFLTSLTLNAAVMWFFY	182
QY	183	GFFKKDFPIAPNPNIIGLFGIVQMLLYVYKDSKIIDDEKSDPVAREATKSKGEVILINI	242
Db	183	GLLIKDKFIAPNPNIIGLFGVAQMLLYMYQGSTTDLPTENQLANKTVDVNEVPIVAVEL	242
QY	243	EDNNSDN 249	
Db	243	PDVGSN 249	

RESULT 3			
ID	Q8LDE6	PRELIMINARY:	PRT: 258 AA.
AC	Q8LDE6:		
DT	01-OCT-2002	(TREMBLrel. 22, Created)	
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE	Similar to MCN3 protein.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid 1; Brassicales; Brassicaceae; Arabidopsids.		

Query	DB	Score	Length	Matches	Conservative	Mismatches	Gaps
1	NCBI TaxID=3702;	52.0%	258	136	48	1	1
2	SEQUENCE FROM N.A.	55.1%	258	136	48	1	1
3	Medline=22088475; PubMed=12093376;	55.1%	258	136	48	1	1
4	Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salberg S.L.;	55.1%	258	136	48	1	1
5	"Full-length messenger RNA sequences greatly improve genome annotation.";	55.1%	258	136	48	1	1
6	Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).	55.1%	258	136	48	1	1
7	SEQUENCE FROM N.A.	55.1%	258	136	48	1	1
8	Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;	55.1%	258	136	48	1	1
9	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	55.1%	258	136	48	1	1
10	EMBL: AY086047; AAM63257.1; -.	55.1%	258	136	48	1	1
11	GO: GO:0016020; C:membrane; IPA.	55.1%	258	136	48	1	1
12	InterPro: IPR004316; MCN3_glv.	55.1%	258	136	48	1	1
13	Pfam: PF03083; MCN3_glv; 2.	55.1%	258	136	48	1	1
14	SEQUENCE 258 AA; 28716 MW; 0C58F852C586AB4F CRC64;	55.1%	258	136	48	1	1
15	Query Match	52.0%	258	136	48	1	1
16	Best Local Similarity	55.1%	258	136	48	1	1
17	Matches	136	258	136	48	1	1
18	Conservative	48	258	136	48	1	1
19	Mismatches	62	258	136	48	1	1
20	Gaps	1	258	136	48	1	1
21	NCBI TaxID=3702;	52.0%	258	136	48	1	1
22	SEQUENCE FROM N.A.	55.1%	258	136	48	1	1
23	Medline=22088475; PubMed=12093376;	55.1%	258	136	48	1	1
24	Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salberg S.L.;	55.1%	258	136	48	1	1
25	"Full-length messenger RNA sequences greatly improve genome annotation.";	55.1%	258	136	48	1	1
26	Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).	55.1%	258	136	48	1	1
27	SEQUENCE FROM N.A.	55.1%	258	136	48	1	1
28	Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;	55.1%	258	136	48	1	1
29	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	55.1%	258	136	48	1	1
30	EMBL: AY086047; AAM63257.1; -.	55.1%	258	136	48	1	1
31	GO: GO:0016020; C:membrane; IPA.	55.1%	258	136	48	1	1
32	InterPro: IPR004316; MCN3_glv.	55.1%	258	136	48	1	1
33	Pfam: PF03083; MCN3_glv; 2.	55.1%	258	136	48	1	1
34	SEQUENCE 258 AA; 28716 MW; 0C58F852C586AB4F CRC64;	55.1%	258	136	48	1	1
35	Query Match	52.0%	258	136	48	1	1
36	Best Local Similarity	55.1%	258	136	48	1	1
37	Matches	136	258	136	48	1	1
38	Conservative	48	258	136	48	1	1
39	Mismatches	62	258	136	48	1	1
40	Gaps	1	258	136	48	1	1
41	NCBI TaxID=3702;	52.0%	258	136	48	1	1
42	SEQUENCE FROM N.A.	55.1%	258	136	48	1	1
43	Medline=22088475; PubMed=12093376;	55.1%	258	136	48	1	1
44	Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salberg S.L.;	55.1%	258	136	48	1	1
45	"Full-length messenger RNA sequences greatly improve genome annotation.";	55.1%	258	136	48	1	1
46	Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).	55.1%	258	136	48	1	1
47	SEQUENCE FROM N.A.	55.1%	258	136	48	1	1
48							

SQ SEQUENCE 268 AA; 30081 MW; 3ED039B2FAEF148E CRC64;
 Query Match 48.5%; Score 656; DB 2; Length 268;
 Best Local Similarity 48.5%; Pred. No. 8,4e-44;
 Matches 129; Conservative 54; Mismatches 55; Indels 28; Gaps 6;
 QY LSPFGLGIVGFMVFLAPVPTFYKIKRKSEGVQAIIPYVVALFSAGLLYYAVALRN 68
 DB LATFGMLGVISFLVFLAPISFYRIYKKSSTEGFQSLVLAALSSMLMLYALIKD 67
 QY AYLVISNGFGCAIELTYISLFLFYAPRKSKIFTGMLM-LLELGALGMVPIITYLLAEGS 127
 DB AFLITINSGCVETIYIILYIYAPRADANLTFKLISMANTGSPALLIIVTNVAVHGP 127
 QY 128 HRVIVGICAINVAVPAAPLSIMROYIKTSVEFMPTLSFLTLCATMFFYGFKK 187
 DB 128 LRVQVIGMVCVSLSVFAAPLSIVAQVARTKSVFEMFPLISFTLTLSATMFGYGFKK 187
 QY 188 DFYIAPNIIIGFLFGIYQMLLYFYVXD-SKRIDDEKSDVREATSKSKEGEVILI----- 240
 DB DITCIXLPNVIGXVGLGIIQMLLYIYRNGEKAKKEKKAPI-BPPKS-----IVITQLE 241
 QY 241 -----NIEDNSDNALQSMEDFS 259
 DB 242 KIEQEKKNKDDNE-----EKDKS 260
 RESULT 5
 ID Q6K602 PRELIMINARY; PRT; 319 AA.
 AC Q6K602;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Putative nodulin 3.
 GN Name=OJ1789 D08.23;
 OS Oryza sativa (Japanese cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriharctideae; Oryzaceae; Oryza.
 ON NCBI_Taxid=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005299; BAD2345.1; -.
 DR InterPro; IPR004316; MCN3_slv.
 DR Pfam; PF03083; MCN3_slv; 2.
 SQ SEQUENCE 319 AA; 34964 MW; 308075F4787795CA CRC64;
 Query Match 47.8%; Score 647; DB 2; Length 319;
 Best Local Similarity 50.4%; Pred. No. 5.1e-43;
 Matches 116; Conservative 53; Mismatches 55; Indels 6; Gaps 2;
 QY 10 SFIFGLIGNIVSFMVFLAPVPTFYKIKRKSEGVQAIIPYVVALFSAGLLYYAVALRN 69
 DB AFTFGILGNISLWVFLAPISFYRIYKKSSTEGFQSLVLAALSSMLMLYALIKD 71
 QY 70 YLVISNGFGCAIELTYISLFLFYAPRKSKIFTGMLM-LLELGALGMVPIITYLLAEGS 128
 DB ELVITINSGCVETIYIILYIYAPRADANLTFKLISMANTGSPALLIIVTNVAVHGP 127
 QY 129 RVMIVGICAINVAVPAAPLSIMROYIKTSVEFMPTLSFLTLCATMFFYGFKK 188
 DB 132 RVHVLGICAVAVSVFAAPLSIRLIRITKSVFEMFPLISFTLTLSATMFGYGFKK 191
 QY 189 FYIAPNIIIGFLFGIYQMLLYFYVXD-SKRIDDEKSDVREATSKSKEGEVILI----- 238
 DB 192 VFVALPVLGVFVGAQMLYMAVRSKPLVASSSSAVVA-----GLEI 236
 RESULT 6
 ID Q8LAGO
 AC Q8LAGO;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Senescence-associated protein (SAG29).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation."
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087836; AAM65389.1; -.
 DR GO: GO:0016020; C.membrane; IEA.
 DR InterPro; IPR002114; HPR_Serp_S.
 DR InterPro; IPR004316; MCN3_slv.
 DR Pfam; PF03083; MCN3_slv; 2.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
 SQ SEQUENCE 292 AA; 32919 MW; 4D92FCA710412P55 CRC64;
 Query Match 46.1%; Score 623.5; DB 2; Length 292;
 Best Local Similarity 43.9%; Pred. No. 3.4e-41;
 Matches 119; Conservative 58; Mismatches 63; Indels 31; Gaps 4;
 QY 9 LSPFGLGIVGFMVFLAPVPTFYKIKRKSEGVQAIIPYVVALFSAGLLYYAVALRN 68
 DB LATFGILGNISFLVFLAPVPTFYRIYKKSSTEGFQSLVLAALSSMLMLYALIKD 69
 QY 69 AYLVISNGFGCAIELTYISLFLFYAPRKSKIFTGMLM-LLELGALGMVPIITYLLAEGS 127
 DB AFLITINSGCVETIYIILYIYAPRADANLTFKLISMANTGSPALLIIVTNVAVHGP 129
 QY 128 H-RVIVGICAINVAVPAAPLSIMROYIKTSVEFMPTLSFLTLCATMFFYGFKK 186
 DB 130 PLOVSVLGVICAVAVSVFAAPLSIMROYIKTSVEFMPTLSFLTLSAVVMFAVGLPL 189
 QY 187 KDFYIAPNIIIGFLFGIYQMLLYFYVXD-SKR----- 218
 DB 190 NDCIAPNVGVGLDQVLYLVYRNSNEPEKINSSEBOLKSLVMSPLGVSEVHY 249
 QY 219 DDEKSDPVREATSKSKEGEVILIINIEDNSDN 249
 DB 250 VTESVDPLSEAV-HHEDLSKVTKEEPSIEN 279
 RESULT 7
 ID Q9FY94
 AC Q9FY94;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Putative senescence-associated protein SAG29 (SAG29).
 GN Name=TI9L5 130; Synonyms=AtSg13170;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

ID Q8LAGO PRELIMINARY; PRT; 292 AA.
 AC Q8LAGO;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Senescence-associated protein (SAG29).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation."
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087836; AAM65389.1; -.
 DR GO: GO:0016020; C.membrane; IEA.
 DR InterPro; IPR002114; HPR_Serp_S.
 DR InterPro; IPR004316; MCN3_slv.
 DR Pfam; PF03083; MCN3_slv; 2.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
 SQ SEQUENCE 292 AA; 32919 MW; 4D92FCA710412P55 CRC64;
 Query Match 46.1%; Score 623.5; DB 2; Length 292;
 Best Local Similarity 43.9%; Pred. No. 3.4e-41;
 Matches 119; Conservative 58; Mismatches 63; Indels 31; Gaps 4;
 QY 9 LSPFGLGIVGFMVFLAPVPTFYKIKRKSEGVQAIIPYVVALFSAGLLYYAVALRN 68
 DB LATFGILGNISFLVFLAPVPTFYRIYKKSSTEGFQSLVLAALSSMLMLYALIKD 69
 QY 69 AYLVISNGFGCAIELTYISLFLFYAPRKSKIFTGMLM-LLELGALGMVPIITYLLAEGS 127
 DB AFLITINSGCVETIYIILYIYAPRADANLTFKLISMANTGSPALLIIVTNVAVHGP 129
 QY 128 H-RVIVGICAINVAVPAAPLSIMROYIKTSVEFMPTLSFLTLCATMFFYGFKK 186
 DB 130 PLOVSVLGVICAVAVSVFAAPLSIMROYIKTSVEFMPTLSFLTLSAVVMFAVGLPL 189
 QY 187 KDFYIAPNIIIGFLFGIYQMLLYFYVXD-SKR----- 218
 DB 190 NDCIAPNVGVGLDQVLYLVYRNSNEPEKINSSEBOLKSLVMSPLGVSEVHY 249
 QY 219 DDEKSDPVREATSKSKEGEVILIINIEDNSDN 249
 DB 250 VTESVDPLSEAV-HHEDLSKVTKEEPSIEN 279
 RESULT 7
 ID Q9FY94
 AC Q9FY94;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Putative senescence-associated protein SAG29 (SAG29).
 GN Name=TI9L5 130; Synonyms=AtSg13170;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RA EMBL; AL313711; CAC05445.1; -
RA EMBL; AY045949; AAK76623.1; -
RA EMBL; AY113934; AAM44982.1; -
RA GO; GO:0016020; C:membrane; IEA.
RA InterPro; IPR002114; HPR Serp S.
RA InterPro; IPR004316; MCN3 sly.
RA Pfam; PF01083; MCN3 sly; 2.
RA PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
SQ SEQUENCE 292 AA; 32936 MW; 4C3826F6D3A845D5 CRC64;
Query Match 46.1%; Score 623.5; DB 2; Length 292;
Best Local Similarity 43.9%; Pred. No. 3,4e-41;
Matches 119; Conservative 58; Mismatches 63; Indels 31; Gaps 4;
QY 9 LSPFGLGIVSNFVFLAPPTPTKYKRSSEGYQALIPVVALFSAGLILYAYIRKN 68
DB 10 LAFIFGLIGNVISFLVFLAPVPTFYRIYKRKSTESFQSLPYQVSLFSCMLWLYALTKD 69
QY 69 AYLVSINGFGCALEIYITSLFLFYAPRKSKIPTGMLML-LELGALGVNMPITLLAEGS 127
DB 70 AFLIITINSFGCVVETLYIAFPAYATREKRISAMKLFIAINVVAPPSLILWVTHFVVKTP 129
QY 128 H-RVMIYVGMICAAINAVFAAPLISIMROVITKTSVEFMPFTLSFLTCATMWFYGF 186
DB 130 PLQSVLGMICVAVLSVFAAPLMIIVARVITKTSVEFMPFTLSFLTISAMWAFYGLFL 189
QY 187 KDFIAPFNITIGFLPGIVQMLLYVYKDSK-----I 218
DB 190 NDICIAIPNVVGFYGLQWLVYVYRNSNEKPKINSSEQQLKSIVMSPLGVSEVHPV 249
QY 219 DDEKSDPVRBATKSGEVEIINIEDNSN 249
DB 250 VTESVDPLEAV-HHEDLSKVTKVEEPIEN 279
RESULT 8
Q9SNM5 PRELIMINARY; PRT; 289 AA.
AC Q9SNM5;
DT 01-MAY-2000 (TRENBLrel. 13; Created)
DT 01-MAY-2000 (TRENBLrel. 13; Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27; Last annotation update)
DE Putative MTN3 protein (AT3g48740/78P19_250).
GN Name=78P19.250; Synonyms=At3g48740;
OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
RN [11]
RP SEQUENCE FROM N.A.
RA Choinsene N., Robert C., Brottier P., Wincker P., Catolico L., K.,
RA Artiguenave F., Saurin W., Weissendach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
RA Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
RA Theologis A., Ecker J.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [17]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [18]
RP SEQUENCE FROM N.A.
RA EMBL; AL13315; CAB62363.1; -
RA EMBL; AY070412; CAB49908.1; -
RA EMBL; AY078041; AAL77742.1; -
RA EMBL; AY096594; AAM20244.1; -
RA EMBL; AF361825; AAK32837.1; -
RA EMBL; AF419559; AAL31891.1; -
DR PIR; T46218; T46218.


```

QY      MAOLRADDDLSPIFGLLGNIVSFMVFLAAPPTPYKTYKRSKSEGOALPYWMLPSACILL 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MAMTR-ESMAFVGGIIGNISFAVFLSLPPTTYVLFKKKSGEGQALPYVALSAAHLMI 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 YVAYL-RKNAYLIVSINGFCALIELTYLSLEFLVAPRSKIIFT-GWMLLELGAIGVMP 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      60 YVAFVVRBSALLLITINTFGIVESAYIIMFLYAPARKQRISTIKLLLLNVPFGGAMLL 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      119 IYTLAEGSRWNIWICAIINVAVFAAPISIMQVTKTSVEMFMPETLSLFTLTATM 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      120 STLYSKGAKRLIIMICLVPNISVFAAPLVISKVRSSVSVEIMPFSLFTLIYAM 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      179 WFFYGFKKDQFYIAPENILGFLFGIVQMLFLVYDYSKRIDEDKSDPYREATKSKEGVEI 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      180 WFFYGLLRDYVALPNTLGFFVGLIOMVVYLIYEN-----ATPVAA-EMKQQL 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      239 -----IINIEDNSDN 249
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      230 SGGHIIIDVVKIGTDS 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 11

ID	PRELIMINARY:	PRT:	285 AA.
OC	082587;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Putative MEN3 protein.		
GN	Name=MEN3; Synonyms=At5g23660;		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RL	Cheong J.-J.;		
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20181125; PubMed=10718197;		
RA	Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,		
RA	Tobara S.;		
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence		
RT	features of the regions of 3,076,755 bp covered by sixty P1 and TrAC		
RT	clones.";		
RL	DNA Res. 7:31-63(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,		
RA	Goldsmith A.D., Lee J.M., Quach H.L., Tortum M., Yu G., Bowser L.,		
RA	Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,		
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,		
RA	Mitanda M., Natusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,		
RA	Sei M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,		
RA	Theologis A.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,		
RA	Tortum M., Yu G., Brookes S., Chao Q., Chen H., Karlin-Neumann G.,		
RA	Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,		
RA	Southwick A., Davis R.W., Ecker J.R., Theologis A.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RA	Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,		
RA	Deng J.M., Goldsmith A.D., Lee J.M., Ondera C.S., Quach H.L.,		
RA	Tang C., Tortum M., Wu H.C., Yamamura Y., Yu G., Bowser L.,		
RA	Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,		
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,		
RA	Meyers M.C., Miranda M., Natusaka M., Nguyen M., Palm C.J.,		

RA Sakurai T., Satou M., Seki M., Shimizu P., Southwick A., Shinozaki K.,
 RA Davis R.W., Eckert J.R., Theologis A.;
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF095641; AAC64192.1; -
 DR EMBL; AB025633; BAA97235.1; -
 DR EMBL; AY057575; AAL09814.1; -
 DR EMBL; AY059108; AAL15214.1; -
 DR EMBL; AY116672; AAM47150.1; -
 DR PIR; T51837; T51837.
 DR GO; GO:0016020; C:membrane; IBA.
 DR InterPro; IPR004316; SLV3 SLV.
 DR Pfam; PF03083; MGN3_slv 2.
 DR Q0 SEQUENCE 285 AA; 3146 MM; E18CD08B1D247B03 CRC64;

Query Match

Query Match	45.7%;	Score 618;	DB 2;	length 285;
Best Local Similarity	47.1%;	Pred. No. 8.9e-41;		
Matches 123;	Conservative	54;	Mismatches 62;	Indels 22;
			Gaps	4

Qy	10	SFIFGLGNGISFVWFLAPVPTFKIYKRKSEGGQALPVMWALFSAQLLLYYAALRNKA	69
Db	11	AFVGGGLGNLISFAVLSFVPTFKIRICCKKTBEGQSLPIYVALLFSANLMLYYAQRKDV	70
Qy	70	YLIVSINGFCALIELTYISLFLFYAPRKSKITFT-GWLMLELGAIGWMPITLYLLAESGH	128
Db	71	FLTLTINSFGCFITETIYISIFVAASKAKRMILTYKLLINMNFGEPCLLILLCQFLAKGTT	130
Qy	129	RVMIVGMICAMINAVFAAPLSIMROYKTKTSVEMPTLSLPLTLCTAMMFYGFPPKD	188
Db	131	RAKTIIGGICVGSFSCVCPAAPLSIRIYAKTSSVEYMPSSLTLTISAVIMLLYGLAKD	190
Qy	189	FYIAFPNLIGLFSGIVQMLLYFYVK-----DSKRIDKESDPVREAT-KSE	234
Db	191	IYVAFPNVIGVILGALQWILYVYVKCKTSPDLVEKLEAAKTLPEVSIWMYKLGTLTSPE	250
Qy	235	GVEIIT-----NIEDNSD	248
Db	251	PVALTVASVNTGCNCDRNAE	271

RESULT 12

PT	Q8LAZ2.	PRELIMINARY;	PT;	294 AA.
AC	Q8LAZ2.			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	MCN3-like protein.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
CC				
CC	NCBI_TaxID=3702;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=22088475; PubMed=12093376;			
RX	Haas B.J., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N., Feldman K.A., Flavell R.B., White O., Salzberg S.L.;			
RA	"Full-length messenger RNA sequences greatly improve genome annotation".			
RT				
RL	Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).			
RP				
RN	SEQUENCE FROM N.A.			
RA	Brayer V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldman K.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY087516; AAM65058.1; -			
DR	GO: GO:0016020; C:membrane; IEA.			
DR	InterPro: IPR004316; MCN3_glv.			
DR	pfam; PF03083; MCN3_glv; Z.			
SO	SEQUENCE 294 AA; 32503 MW; 6479486E5A0F0B84 CRC64;			
Query Match	43.6%;	Score 590;	DB 2;	Length 294;
Best Local Similarity	46.6%;	Pred. NO. 1.5e-36;		

Matches 126; Conservative 46; Mismatches 57; Indels 30; Gaps 6;

QY 10 SFFGLGNIVSMVFLAPVPTFYKTKYKRSSEGYQAIPYVALPSAGLLYYAARLN-N 68
 DB 9 AFVFGILGNISFVFLAPVPTFYKTKYKRSSEGYQAIPYVALPSAGLLYYAARLN-N 68
 QY 69 AYLIVSINGFCALBETIYISLFLFYAPRKSIFT---GWLMLLEGLALGMVPIITYLLA 124
 DB 69 AFLILITINAGCVIETIYIVLFPVSANKTRISTLKVGLNLFGLFAIIVLVCZ---LLT 125
 QY 125 EBSHRVIMVGMICAINAVFAAPLSIMROVITKTSVEFMPFTLSLFLTCATMFFPYG 184
 DB 126 KSGTREVIGGICVGSVSFAAPLSIMRVVTRSGVEFMPFTLSLFLTISAVTWLFYGL 185
 QY 185 FKDFEIAFPNIGLFLGVOMLLFYVYKSDKRIIDDEKSDPVREATKSGEVEIINIED 244
 DB 186 AIKDFYVALPNNVGAFLGAVQMILYIIFKYKTPVAQKTD-----KSK----- 228
 QY 245 DNSDNALQSMEXKDFSLRT 263
 DB 229 DVSDHSI-----DIKLT 242

RESULT 13

Q9FGQ2 PRELIMINARY; PRT; 294 AA.

AC 09FGQ2; 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE MCN3-like protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kaneo T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.; Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB025617; BAB08903.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR004316; MCN3_glv.
 DR Pfam; PF03083; MCN3_glv; 2.
 SQ SEQUENCE 294 AA; 32503 MW; 26D88F65398D0DAE CRC64;

Query Match 43.6%; Score 590; DB 2; Length 294;
 Best Local Similarity 48.6%; Pred. No. 1.5e-38;
 Matches 126; Conservative 46; Mismatches 57; Indels 30; Gaps 6;

QY 10 SFFGLGNIVSMVFLAPVPTFYKTKYKRSSEGYQAIPYVALPSAGLLYYAARLN-N 68
 DB 9 AFVFGILGNISFVFLAPVPTFYKTKYKRSSEGYQAIPYVALPSAGLLYYAARLN-N 68
 QY 69 AYLIVSINGFCALBETIYISLFLFYAPRKSIFT---GWLMLLEGLALGMVPIITYLLA 124
 DB 69 AFLILITINAGCVIETIYIVLFPVSANKTRISTLKVGLNLFGLFAIIVLVCZ---LLT 125
 QY 125 EBSHRVIMVGMICAINAVFAAPLSIMROVITKTSVEFMPFTLSLFLTCATMFFPYG 184
 DB 126 KSGTREVIGGICVGSVSFAAPLSIMRVVTRSGVEFMPFTLSLFLTISAVTWLFYGL 185
 QY 185 FKDFEIAFPNIGLFLGVOMLLFYVYKSDKRIIDDEKSDPVREATKSGEVEIINIED 244
 DB 186 AIKDFYVALPNNVGAFLGAVQMILYIIFKYKTPVAQKTD-----KSK----- 228
 QY 245 DNSDNALQSMEXKDFSLRT 263
 DB 229 DVSDHSI-----DIKLT 242

RESULT 14

Q9SM25 PRELIMINARY; PRT; 281 AA.

AC 09SM25; 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE MCN3-like protein.
 GN Name=F13M23.150; Synonym=AT4G25010;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Medler H., Medler E., Wambutt R., Hebeisel J., Mewes H.W.,
 RA Mayer K.F.X., Scheller C.; Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Medler H., Medler E., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035523; CAB36743.1; -
 DR EMBL; AL161562; CAB79410.1; -
 DR PIR; T05522; T05522.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR004316; MCN3_glv.
 DR Pfam; PF03083; MCN3_glv; 2.
 SQ SEQUENCE 281 AA; 30969 MW; D01DA2649AC9B92 CRC64;

Query Match 41.7%; Score 564.5; DB 2; Length 281;
 Best Local Similarity 50.8%; Pred. No. 1.5e-36;
 Matches 121; Conservative 39; Mismatches 65; Indels 13; Gaps 5;

QY 9 LSFFGLGNIVSMVFLAPVPTFYKTKYKRSSEGYQAIPYVALPSAGLLYYAARLN-N 68
 DB 8 LAVTRGVGNISFVFLAPVPTFYKTKYKRSSEGYQAIPYVALPSAGLLYYAARLN-N 67
 QY 69 AYLIVSINGFCALBETIYISLFLFYAPRKSIFT---GWLMLLEGLALGMVPIITYLL 123
 DB 68 AFLILITINAGCVIETIYIVLFPVSANKTRISTLKVGLNLFGLFAIIVLVCZ---LL 124
 QY 124 AEGSHRVIMVGMICAINAVFAAPLSIMROVITKTSVEFMPFTLSLFLTCATMFFPYG 183
 DB 125 TKSNSEKVLGICVGSVSFAAPLSIMRVVTRSGVEFMPFTLSLFLTISAVTWLFYGL 184
 QY 184 FKDFEIAFPNIGLFLGVOMLLFYVYKSDKRIIDDEKSDPVREATKSGEVEIINIED 239
 DB 185 AIKDFYVALPNNVGAFLGAVQMILYIIFKYKTPVAQKTD-----KIVSDHSIMV 239

RESULT 15

Q6YZF3 PRELIMINARY; PRT; 307 AA.

AC 06YZF3; 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Putative MCN3.
 GN Name=P0702C09.33; Synonym=OSJNBa0033D24.17;
 OS Oryza sativa (japanese cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;

```
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005528; BAD13168.1; -.
DR EMBL; AP005439; BAD13102.1; -.
DR InterPro: IPR004316; MEN3_glv.
DR Pfam; PF03083; MEN3_glv; 2.
SQ SEQUENCE 307 AA; 32978 MW; 6E505D8DA701B664 CRC64;
```

Query Match 39.8%; Score 539; DB 2; Length 307;

Best Local Similarity 45.4%; Pred. No. 1.6e-34;

Matches 104; Conservative 49; Mismatches 70; Indels 6; Gaps 2;

```
QY 14 GLUGNIVSPMVFLAPVPTFYKIKRKSSEGYQALPYMVALFSAGLLLYAYLRNAYLV 73
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 17 GVAIGNIISFLVFLAPVATPFLQVYKKKSTGGYSSVPYVALFSSVLWIFVALVKTNRP 76
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 74 SINGEGCAIETVYSLFLFYAPRKSIFP-CMLMLELGLGVMPTIYLLAEGSHRMT 132
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 77 TINAFGCGVEAAYIVLVYAPRRARLRTLAFLLLDVAAPALIVTTLVIVPRHQVKF 136
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 133 VGMICAIINAVFAAPLISIMROVIKTSVEFMPTLSLFLTLCAWMFFYGFKKDFYIA 192
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 137 LGSVCLAFSMAVFAVAPLSIIFKVIKTSVEFMPIGLSVCLTISAVAMFCYGLFTKDPY 196
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 193 FPNILGFLFGIVQMLLFFVYKDSKR----IDDEKSDPVREATKSKEGV 236
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 197 YPNVGGFFFSCVQMGLYFYWRKPRNTAVLPPTSDMSPISAATAATQRV 245
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

Search completed: December 24, 2004, 20:43:08

Job time : 138 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 24, 2004, 20:29:56 ; Search time 52 Seconds
(without alignment)

490.335 Million cell updates/sec

Title: US-09-743-885A-1

Perfect score: 1353

Sequence: 1 MAQLADDSFTFGLGNIV.....NSDNALQSMKOPSRRLTSK 265

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	704.5	52.1	258	2 F84812	similar to MEN3 pr
2	622	46.0	289	2 T46218	MTN3-like protein
3	618	45.7	285	2 T51837	MTN3 homolog [impo
4	564.5	41.7	281	2 T05522	hypothetical prote
5	350	25.9	202	2 F86347	hypothetical prote
6	325	24.0	238	2 T04280	hypothetical prote
7	319.5	23.6	249	2 T01891	hypothetical prote
8	291.5	21.5	238	2 A71425	hypothetical prote
9	243	18.0	355	2 T19016	hypothetical prote
10	233.5	17.3	686	2 A71607	MEN3/RAG1P-like p
11	220	16.3	250	2 T26725	hypothetical prote
12	216	16.0	221	2 JC4761	recombinational acti
13	213.5	15.8	233	2 T31865	hypothetical prote
14	209.5	15.5	299	2 T32982	hypothetical prote
15	146	10.8	224	2 T32655	hypothetical prote
16	114.5	8.5	300	2 S36430	hypothetical prote
17	114	8.4	546	1 B24707	NADH2 dehydrogenas
18	112	8.3	546	2 A69890	hypothetical prote
19	109	8.1	808	2 T16564	hypothetical prote
20	108.5	8.0	567	2 B81408	probable thiol-dis
21	108.5	8.0	687	2 C71849	carbon starvation
22	108	8.0	583	2 T48473	amino acid transpo
23	107.5	7.9	687	2 H64665	carbon starvation
24	106	7.8	475	2 B29606	methylesterase
25	105.5	7.8	361	2 D89869	conserved hypochet
26	104.5	7.7	228	2 D90513	hypothetical prote
27	103.5	7.6	489	2 G90402	hypothetical prote
28	102	7.5	253	2 E75055	hypothetical prote
29	100.5	7.4	229	2 T24122	hypothetical prote

30	100.5	7.4	356	2 B97822	probable permease
31	100	7.4	444	2 T12297	NADH2 dehydrogenas
32	99.5	7.4	399	2 AF3349	hypothetical prote
33	98.5	7.3	395	2 H81390	probable integral
34	98.5	7.3	567	2 D65043	hypothetical prote
35	98.5	7.3	567	2 T08653	hypothetical prote
36	98.5	7.3	829	2 A99960	hypothetical prote
37	98	7.2	202	2 F72008	CT852 hypothetical
38	97.5	7.2	201	2 H97219	uncharacterized co
39	97.5	7.2	508	2 D90567	hypothetical prote
40	97.5	7.2	596	2 S46001	probable amino aci
41	97	7.2	245	2 C30010	hypothetical ORF-6
42	97	7.2	380	2 D64352	hypothetical prote
43	97	7.2	583	2 AH1151	glycerophosphoryl
44	96.5	7.1	422	2 AC1189	phosphotransferase
45	96.5	7.1	433	2 T11162	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

F84812 similar to MEN3 protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear creas)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: F84812

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shua, T.P.; Benito, M.T.; Town, C.D.; Fujita, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;

ause, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MID:20083487; PMID:1061197

A/Accession: F84812

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-258 <STO>

A/Cross-references: UNIPROT:Q92V02; GB:AE002093; NID:G328090; PIDN:AMC79616.1; GSPDB:GNK

C/Gene: At2g39060

A/Map position: 2

Query Match 52.1%; Score 704.5; DB 2; Length 258;

Best Local Similarity 55.1%; Pred. No. 3.8e-55;

Matches 136; Conservative 48; Mismatches 62; Indels 1; Gaps 1;

QY 4 LRADDSFTFGLGNIVSPVFLAPVPTFYIKRKSSEGOAIPIYVALFSAGLLLYA 63

3 LKVEHIAFLFGLGNIVSFGVFLSPVPTFYIKRKSSEGOAIPIYVALFSAGLLLYA 62

QY 64 YLRKNAVLYVINGFGCAIFLYTISLFLRYAPPKSKIFGWLMLL-ELGALGVMPITLY 122

63 IMKTHAVLYIISITFCFPIEISYLFYIYAPREAKISTLKLIVINIGLGLILLVNL 122

QY 123 LAEGSHRWIVGVICAIWAVPAAPLSTIMROVYIKRKSSEVPEPTSLFTLCATMFFY 182

123 LVPKQHRVSTGVWCAVSLAVPASPLSVKRYIKRKSSEVPEPTSLFTLCATMFFY 182

QY 183 GFPKDFYIAFPNIIFLFGIVQMLLYFYVYKDSKRIIDKSDPVRATSKSEGEVITINI 242

183 GLIKDKFTAMPILDFLFGVAQMILYMYVQGSTKTDLPFTENGLANKTIDVNEVPIYAVEL 242

QY 243 EDDNSDN 249

243 PDVGSND 249

Db 243 PDVGSND 249

RESULT 2

T46218

MTN3-like protein - Arabidopsis thaliana

N/Alternate names: protein T8P19.250

C/Species: Arabidopsis thaliana (mouse-ear creas)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46218
R:Choiame, N.; Robert, C.; Brothier, P.; Mincker, P.; Catcollis, L.; Attiguenave, F.; Se
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223008
A:Accession: T46218
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <CHO>
A:Cross-references: UNIPROT:Q9SMN5; EMBL:AL133315
A:Experimental source: cultivar Columbia, BAC clone T8P19
C:Genetics:
A:Map position: 3
A:introns: 18/1; 30/2; 100/3; 154/3; 194/3
A:Note: T8P19.250

Query Match 46.0%; Score 622; DB 2; Length 289;
Best Local Similarity 47.9%; Pred. No. 9.2e-48;
Matches 126; Conservative 46; Mismatches 63; Indels 28; Gaps 4;

QY 10 SPFGGLGNIVSFMWFLAPVPTFYKIKRKSEGYOAIPIYVWALFSAGLLYAYALRNA 69
Db 11 AFVFGGLGNLISFAVFLSPVPTFYRIWKKTTEGFSQIPYVVALFSATLWLYATOKDV 70
QY 70 YLIASINGGCAIETLYISLFLFYAPRKSIFT-GWMLLELGLAGWMPITLYLAAESH 128
Db 71 FLVLTINAFGCFIETIYISMLATAFKPARMLTKMLLMMFGFCALILCOFLVKGAT 130
QY 129 RWMIVGICAIINAVFAPLISIMROVITKTSVEFMPTLSLFTLTCAIWMFFYGFPRKD 188
Db 131 RAKIIGGICGVFSVCVFAAPLSIRTVIKTSVEVEMPSLSLTITISAVIWLVLGLAKD 190
QY 189 FYIAFPNLTGFLGIVQMLLYFYTK-----DSKRIIDEX-----SDP- 225
Db 191 IYVAFPNVLGFGALGLQMLILYVVKYCKTSPHLGKEVEAKLPEVSLMDKLGTVSSPE 250
QY 226 ----VREATSKSEGEIITIED 244
Db 251 PISVVRQANKCTCGNDRAIED 273

RESULT 3
T51837
MTN3 homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51837
R:Cheong, J.J.
submitted to the EMBL Data Library September 1998
A:Description: An Arabidopsis cDNA clone encoding a protein homologous to Medicago truncatula
A:Reference number: 225460
A:Accession: T51837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-285 <CHE>
A:Cross-references: UNIPROT:O82587; EMBL:AF095641; PIDN:AAC64192.1
C:Genetics:
A:Note: MTN3

Query Match 45.7%; Score 618; DB 2; Length 285;
Best Local Similarity 47.1%; Pred. No. 2e-47;
Matches 123; Conservative 54; Mismatches 62; Indels 22; Gaps 4;

QY 10 SPFGGLGNIVSFMWFLAPVPTFYKIKRKSEGYOAIPIYVWALFSAGLLYAYALRNA 69
Db 11 AFVFGGLGNLISFAVFLSPVPTFYRIWKKTTEGFSQIPYVVALFSATLWLYATOKDV 70
QY 70 YLIASINGGCAIETLYISLFLFYAPRKSIFT-GWMLLELGLAGWMPITLYLAAESH 128
Db 71 FLVLTINAFGCFIETIYISFVAFASKKAPMLTKVALLMMNFGFCILILCOFLAKGT 130
QY 129 RWMIVGICAIINAVFAPLISIMROVITKTSVEFMPTLSLFTLTCAIWMFFYGFPRKD 188
Db 131 RAKIIGGICGVFSVCVFAAPLSIRTVIKTSVEVEMPSLSLTITISAVIWLVLGLAKD 190

QY 189 FFIAPENILGFFFGIYOMLLEFYVK-----DSKRIIDDEKSDPREAT-KSKS 234
DB 191 IYVAFPNVIGFVLGALQMLLYVYVKCKTPSDLVEKLEBAKLPKPSIDMWKGLTINSPE 250

QY 235 GVEIIT-----NIEDNSD 248
DB 251 PVALTVRSVNTCNCDNRNAB 271

RESULT 4
T05522
hypothetical protein F13M23.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05522
R:Bevan, M.; Wedler, H.; Wedler, E.; Wandutt, R.; Hohsels, J.; Mewes, H.W.; Mayer, K.F. et al.
submitted to the Protein Sequence Database, February 1999
A:Reference number: 215419
A:Accession: T05522
A:Molecule type: DNA
A:Residues: 1-281 <BEV>
A:Cross-references: UNIPROT:Q9SW25; EMBL:AL035523
C:Experimental source: cultivar Columbia; BAC clone F13M23
C:Genetics:
A:Map position: 4
A:Introns: 16/1; 28/2; 99/3; 153/3; 193/3
A>Note: F13M23.150

Query Match 41.7%, Score 564.5, DB 2, Length 281;
Best Local Similarity 50.8%; Pred. No. 1.1e-42;
Matches 121, Conservative 39, Mismatches 65, Indels 13, Gaps 5;

QY 9 ISFTIGLGNITSPWVFLAPVPEFYKIKRKSEGGYOAIPYVALPSAGILLYAYAKRN 68
DB 8 LAVTGVGLNITSPVFLAPVPEFYKIKRKSEGGESLPVLSALPSAMLYVALQDGG 67
QY 69 A-LYIVSINGFCAGLELYTISFLFYAPRKSKITFT---GWLMLLELGALGMVPITYLL 123
DB 68 AGFLIITINAVGCFIETITIIIFITANKKARISTLKVGLNPLGPAIILVGE---LL 124

QY 124 AEGSHRWIVMGITCAAINVAVPAAPLSIMROVITKYSVEEMPPTLSLPLTLCATMFPFYG 183
DB 125 TKGSRREKVLGICVGFSCVCPAAPSIMRVVIRTKSVEMPEPSLSLPLTISAITWLFYG 184

QY 184 PFKKQFYIAFPIILGFLGIVOMLLEFYVKDSKR--IDDEKSDPVRRATSKSEVEIT 239
DB 185 LAIKPFVALPNIILGFLGAVQMLLYVYFKYKTPPLVDETEKP--KTVSDHSINMV 239

RESULT 5
P86347
hypothetical protein P24J8.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: P86347
R:Theologis, A.; Ecker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-U.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yi, G.; Frazer, C.W.; Venter, J.C.; Davis, R.W.
Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: P86347
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <STO>
A:Cross-references: UNIPROT:Q9LPL1; GB:AE005172; NID:g9454576; PIDN:AA87899.1; GSPDB:GN C:Genetics:

A:Map position: 1

Query Match 25.9%; Score 350; DB 2; Length 202;

Best Local Similarity 37.2%; Pred. No. 8.8e-24; Matches 77; Conservative 40; Mismatches 82; Indels 8; Gaps 3;

QY 51 VALFSAGLLLYYA--YLKNAVLIVSINGFGCAIELTYISLFLVAPRKSKIFTGWLML 108

DB 1 MTLNCLSLMWGLPFLVSKONTLVTSTNGAVIETTYVILFLFYAPKKEKIKIFGFSC 60

QY 109 ELGALGMNPITYLLAEGSHRWIVGICAINVAFADLSIMROVYIKTSVEFMPFTL 168

DB 61 VLAVFAVALVSLFALQGNRKLFCGLAATVPFSIIIMVASPSIMRLVTKTSVEFMPFTL 120

QY 169 SLFLTCATMMPFYFPGKDFYAFPIIIGFLFGIVGMILLYFYKDSKRIDDEKSDPVRE 228

DB 121 SLFVFCGTSWPFYVGLGRPFVAIPFGFCAIGTLQLILYFCGK--GKSS--AD 174

QY 229 ATKSEGVETIINIEDNSDALQSM 255

DB 175 AQKDEKSEVMEKDEKKONVNGKDDLO 201

RESULT 6

T04280 hypothetical protein F25124.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04280

C:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, March 1999

A:Reference number: 215261

A:Accession: T04280

A:Molecule type: DNA

A:Residues: 1-238 <BEV>

A:Cross-references: UNIPROT:Q9SN64; EMBL:AL049525

A:Experimental source: cultivar Columbia; BAC clone F25124

C:Genetics:

A:Map position: 4

A:Introns: 136/3; 176/3

A:Note: F25124.60

Query Match 24.0%; Score 325; DB 2; Length 238;

Best Local Similarity 36.5%; Pred. No. 1.7e-21; Matches 74; Conservative 43; Mismatches 78; Indels 8; Gaps 5;

QY 30 PTFYKIYKRSSEGYQAIPIYVALFSAAGLLLYYA--LKNNAVLIVSINGFGCAIELTYI 87

DB 7 PTFVRIYKKSVEEYSPILATLINCIVWVLYGLPTVHPDSTLVITINGGILIEIVFL 66

QY 88 SLFLFAAPR-KSKIFTGWLMLLELGAIGMNPITYLLAEGSH-RWIVGICAINVAVF 145

DB 67 TIFPVYCGRQKRLIISAVIAETAFIALVAVLTLOHTTEKRTMSVGIKCVFNNMY 126

QY 146 AAPLSIM--ROYIKTSVEFMPFTLSLFLTCATMMPFYFPGKDFYAFPIIIGFLFG 202

DB 127 ASPLSVWVRKKNVITKTSVEFMPFLSVAGFLNAGVMTIYALMPDFPMALPBGICLFG 166

QY 203 IVQMLLY-FVYKDSKRIDDEKSD 224

DB 187 LAQLILYGAAYKSTKRIMAREN 209

RESULT 7

T01891

hypothetical protein F8M12.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C:Accession: T01891

C:Madson, C.; Graves, T.; Cotton, M.; Modde, T.

submitted to the EMBL Data Library, July 1998

A:Description: The sequence of A. thaliana F8M12.

A:Reference number: 214450

A:Accession: T01891

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-249 <MAD>

A:Cross-references: UNIPROT:O91628; EMBL:AF080118; NID:G3513725; PID:G3513744

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 4

A:Introns: 135/1; 147/3; 187/3

A:Note: F8M12.20

Query Match 23.6%; Score 319.5; DB 2; Length 249;

Best Local Similarity 34.6%; Pred. No. 5.6e-21; Matches 74; Conservative 43; Mismatches 78; Indels 19; Gaps 5;

QY 30 PTFYKIYKRSSEGYQAIPIYVALFSAAGLLLYYA--LKNNAVLIVSINGFGCAIELTYI 87

DB 7 PTFVRIYKKSVEEYSPILATLINCIVWVLYGLPTVHPDSTLVITINGGILIEIVFL 66

QY 88 SLFLFAAPR-KSKIFTGWLMLLELGAIGMNPITYLLAEGSH-RWIVGICAINVAVF 145

DB 67 TIFPVYCGRQKRLIISAVIAETAFIALVAVLTLOHTTEKRTMSVGIKCVFNNMY 126

QY 146 AAPLSIM-----ROYIKTSVEFMPFTLSLFLTCATMMPFYFPGKDFYI 191

DB 127 ASPLSVWVRKKNVITKTSVEFMPFLSVAGFLNAGVMTIYALMPDFPM 186

QY 192 APFNILGFLFGIVGMILLY-FVYKDSKRIDDEKSD 224

DB 187 AIPNGICLFGIALQLILYGAAYKSTKRIMAREN 220

RESULT 8

A71425 hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: Columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C:Accession: A71425

C:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirki,

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weltenegger, T.; Pohl, T.M.; Terry, N.; Giet,

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc

C.; Chaiwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: A71425

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <BEV>

A:Cross-references: UNIPROT:Q23441; GB:297339; NID:G32244901; PID:G327488; PID:G32244949

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 21.5%; Score 291.5; DB 2; Length 298;

Best Local Similarity 32.7%; Pred. No. 2.1e-18; Matches 64; Conservative 36; Mismatches 49; Indels 47; Gaps 5;

QY 8 DLSPFGLGNIVSPWFLAPV-----PTFYKIYKRSSEGYQAIPIYV 51

DB 3 BASFYIGVGNVSVLVSFLVILDRSLIYOTKIRRETFWIKVGRSREYKSLPYIC 62

QY 52 ALPSAGLLLYAYLKNNAVLIVSINGFGCAIELTYISLFLVAPRKSKIFTGWLMLLEL 111

DB 63 TLGSSLMITYGIVTGEYLVSTVNGFGLVETIYVSLFLFYAPRLKTKT-----VDVD 117

QY 112 A-LGMNPITYLLAEGS-----HRVIVGICAINVAVFAPLSIMRVITKTSVEFM 164

DB 118 AMNVVFPPIAAVATSAFEDKMRQSIGFISAGLITMIGSPLSAM----- 165

QY 165 PFTLSLFLTCATMWF 180

A/Accession: J04761
 A/Molecule type: mRNA
 A/Residues: 1-221 <TAG>
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Comment: This protein is a membrane receptor involved in the induction of recombination
 C/Genetics:
 A/Genes: C2.3
 C/Keywords: phosphoprotein
 F/157/Binding site: phosphate (Thr) (covalent) #statue predicted

Query Match 16.8%; Score 216; DB 2; Length 221;
 Best Local Similarity 26.0%; Pred. No. 7.6e-12;
 Matches 47; Conservative 49; Mismatches 73; Indels 12; Gaps 3;

QY 37 KRKSSGYQAIPIYMAVLFSGALLYYARKNAVLIVSINGFCATELTITSLFPAAPR 96
 DB 35 RTSSVDNIQPLPPLTVDNLSWLSGVKLGDTLLI-VNSGAVLQTLVILVLAHSPQ 93
 QY 97 KSKIFGMLLLELALGAWMPITY-----LAEGRHWIVGICAINVAFAAPLST 151
 DB 94 KHGV-----LQATLTLNVLILGYFMLVDPLEARLQGLFCSVFITSMVLSPLAD 147
 QY 152 MROVITKTSVEMFPTLSLFLTCATWMPFYGFPKDGYAFAPNIIIGFLFGIVQMLIFV 211
 DB 148 LAKIVQTKSTQRLSFLITATLFCASWSIYGFRLRDPYAVAPNLPGILTSIRLGFCCK 207
 QY 212 Y 212
 DB 208 Y 208

RESULT 13

T31865
 hypothetical protein C54F6.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T31865
 R/Giesel, C.; Bradshaw, H.
 submitted to the EMBL Data Library, July 1997
 A/Description: The sequence of C. elegans cosmid C54F6.
 A/Reference number: Z21094
 A/Accession: T31865
 A/Molecule type: DNA
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 1-233 <GEI>
 A/Cross-references: UNIPROT:O16448; EMBL:AF016447; PIRN:AA065939.1; GSPDB:GN00023; CESP:
 A/Experimental source: strain Bristol N2; clone C54F6
 C/Genetics:
 A/Genes: C54F6.4
 A/Map position: 5
 A/Intons: 15/2; 41/2; 82/3; 131/3; 171/3

Query Match 15.8%; Score 213.5; DB 2; Length 233;
 Best Local Similarity 25.1%; Pred. No. 1.3e-11;
 Matches 46; Conservative 46; Mismatches 84; Indels 7; Gaps 3;

QY 30 PTRYKTYKRSSGYQAIPIYMAVLFSGALLYYARKNAVLIVSINGFCATELTITSL 89
 DB 16 PICLQIYRQGVHDISGFPLMGTLVLPFWLRGFLN-NVMVLSINCAQIPYAV-FNAP 73
 QY 90 FLFYAPRKSKIFGMLLLELALGAWMPITYLLAEGRHWIVGICAINVAFAAPL 149
 DB 74 FLFYFSKPKRYVTQSLIVITITLMLLHF-----NPNVQPLGFICYLNLITRESPL 128
 QY 150 SINQVITKTSVEMFPTLSLFLTCATWMPFYGFPKDGYAFAPNIIIGFLFGIVQML 209
 DB 129 AGRAVVLDRREVITLPVLCVQLVQCLMNLVGIILQDFLVPYAVGIMISIVQLSTLF 188
 QY 210 FVY 212
 DB 189 LIF 191

RESULT 14

T32982
 hypothetical protein K02D7.5 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T32982
 R/Du, Z.; Magg1, L.
 submitted to the EMBL Data Library, February 1998
 A/Description: The sequence of C. elegans cosmid K02D7.
 A/Reference number: Z21259
 A/Accession: T32982
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-299 <DUZ>
 A/Cross-references: UNIPROT:O45102; EMBL:AF045645; PIRN:AA02609.1; GSPDB:GN00023; CESP:
 A/Experimental source: strain Bristol N2; clone K02D7
 A/Map position: 4
 A/Intons: 25/2; 51/2; 92/3; 141/3; 181/3; 232/1

Query Match 15.5%; Score 209.5; DB 2; Length 299;
 Best Local Similarity 27.3%; Pred. No. 4e-11;
 Matches 57; Conservative 37; Mismatches 96; Indels 19; Gaps 4;

QY 24 VFAPVPTRYKTYKRSSGYQAIPIYMAVLFSGALLYYARKNAVLIVSINGFCATE 83
 DB 20 LFFCGIPICMQIRQCAVGDISGFPLMGVLSFPLRGYGLKMD-YWMIYVNVGACM 78
 QY 84 LTYISLFLFYAPRKSKIFGMLLLELALGAWMPITYLLAEGRHWIVGICAINVA 143
 DB 79 AFYCVFPLIYSLPK-KTFTCOLIVTSTIGVWLIAL-----KPNLDYGVICMTFNIM 132
 QY 144 VFAAPLSTINQVITKTSVEMFPTLSLFLTCATWMPFYGFPKDGYAFAPNIIIGFLFGI 203
 DB 133 NFQAPLAGGVVLKQNEVSTLPMPKCVANFLVSSQCLGNLVSDIYIIPNGIGMFLAI 192
 QY 204 VQMLIFYVYKDSKRIDEKSDPVEATKS 232
 DB 193 VQMLFVVL-----PIRENEKS 209

RESULT 15

T32655
 hypothetical protein K11D12.5 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T32655
 R/Henhaus, J.; Wohldmann, P.; Gilling, B.
 submitted to the EMBL Data Library, December 1997
 A/Description: The sequence of C. elegans cosmid K11D12.
 A/Reference number: Z21207
 A/Accession: T32655
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-224 <HEN>
 A/Cross-references: UNIPROT:O44620; EMBL:AF039047; PIRN:AA094225.1; GSPDB:GN00023; CESP:
 A/Experimental source: strain Bristol N2; clone K11D12
 C/Genetics:
 A/Genes: K11D12.5
 A/Map position: 5
 A/Intons: 46/2; 89/3; 141/3; 181/3

Query Match 10.8%; Score 146; DB 2; Length 224;
 Best Local Similarity 20.5%; Pred. No. 1.3e-05;
 Matches 45; Conservative 47; Mismatches 99; Indels 28; Gaps 8;

QY 22 FMVFLAPVPTRYKTYKRSSGYQAIPIYMAVLFSGALLYYARKNAVLIVSINGFC 79
 DB 13 FSIQFTFLPMFVLDHMKGTADGSSVNFVLPMLVQSFMLRHGYNTNDOTNII-INSIN 71
 QY 80 CALETYISLFLFYAPRKSKIFGMLLLELALGAWMPITYLLAEGRHWIVGICAINVA 138

Db 72 LVFPAYVSAFAYYQP-KRXYLIGQIV--AAALAVKVAFAVVDTHDSASINDAMGMAA 127
QY 139 AINVAVFAAPLISIMRQVYIKTSVEFMP-FTLSLFTLCATWMEFYGFKKDFYIAPNI 196
Db 128 GAQIFSLVSGIYEIKRAISMGTEYIPAGQPAIFTLI--LQWLLPGLHGNQFIASNA 185
QY 197 LGFLPGIVOMLIFYVY-----KDSKRID 219
Db 186 AGLLVNIATLALYFFYPPLTWVPINFNIPQNKDAKVE 224

Search completed: December 24, 2004, 20:44:10
Job time : 53 secs


```
Db      129 KRISVIGMIGLVNLSVFAAPLCTMKRVITKRSVEFMPFSLFPLTINAVMFPYGLLK 188
Qy      188 DFYIAFPNIIGFLFGLIYQMLLFYVYKRSKRIDDEKSDPVEATKSKGEVEIINIEDDN 246
Db      189 DYVALPNIIGFLFGLIYQMLLYLYIRNA-----KPGLEBPTVQGLNHIIIDVAPN 241
```

```
RESULT 2
US-10-425-115-214274
; Sequence 214274, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 214274
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127016C.1.pep
US-10-425-115-214274
```

```
Query Match      49.5%; Score 669.5; DB 17; Length 246;
Best Local Similarity 53.8%; Pred. No. 8,7e-56;
Matches 120; Conservative 52; Mismatches 44; Indels 7; Gaps 2;

Qy      9  LSFIFGLGNIVSFMVFLAPVPFPTKYIKRSGYQAIIPYVVALFSAGLLYYAAYLRKN 68
Db      10  MAFAFGLGNVISMTFLAPLPFPTRYIKRSGTEGFSVPYVALFSAMLMIFYALKSN 69
Qy      69  AYLVISNGFCALIELTYISLFLFYAPRKSRIPTG-WMLLELGCALGMVNPITYLAEGS 127
Db      70  ELLITITNSACVETIETIYIMVLYAPRKAKLFTAKILLNLNGVFGVILLITLLLSAQ 129
Qy      128  HRVMTVGMICAINVAAPLPSIMROVITKRSVEFMPFTLSFLTCATWMPFYGFKK 187
Db      130  RRVVLLGMVCVAFSVFVAPLSIRVTRSVFMPFSLISLTJVSAVVMFLYGLLIK 189
Qy      188  DFYIAFPNIIGFLFGLIYQMLLYFYKDS-----KRIDDEKSD 224
Db      190  DKVALPNIIGFSFGVQVGLYALYRNATPRVPFKVDADGKD 232
```

```
RESULT 3
US-10-425-114-68239
; Sequence 68239, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68239
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Zea mays
```

```
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17025G08_FIL.pep
US-10-425-114-68239
Query Match      48.3%; Score 654; DB 15; Length 299;
Best Local Similarity 52.8%; Pred. No. 3.4e-54;
Matches 121; Conservative 46; Mismatches 50; Indels 12; Gaps 2;
```

```
Qy      10  SFIIFGLGNIVSFMVFLAPVPFPTKYIKRSGYQAIIPYVVALFSAGLLYYAAYLRKN 69
Db      7  AFAFGLGNVISMTFLAPLPFPTRYIKRSGTEGFSVPYVALFSAMLMIFYALKSN 66
Qy      70  YLVISNGFCALIELTYISLFLFYAPRKSRIPTGWM-LLELGCALGMVNPITYLAEGSH 128
Db      67  TPLITITNAGCVETIETIYIMVLYAPRKAKLFTAKIMALLNGVFGVILLITLLFRGSK 126
Qy      129  RVMIVGMICAINVAAPLPSIMROVITKRSVEFMPFTLSFLTCATWMPFYGFKKD 188
Db      127  RVALLGWICVGSFVSFVAPLSIMRVIOTKRSVEFMPFSLISLTJVSAVVMFLYGLLIK 186
Qy      189  FYIAFPNIIGFLFGLIYQMLLYFYVY-----KDSKRIDDEKSDPV 226
Db      187  KYVALPNIIGFIRGVQVGLYVYRNKTPVAAAVGADAGLPSAADHV 235
```

```
RESULT 4
US-10-425-115-214284
; Sequence 214284, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 214284
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127025C.1.pep
US-10-425-115-214284
```

```
Query Match      48.3%; Score 653.5; DB 17; Length 302;
Best Local Similarity 50.4%; Pred. No. 3.8e-54;
Matches 122; Conservative 49; Mismatches 54; Indels 17; Gaps 3;
```

```
Qy      10  SFIIFGLGNIVSFMVFLAPVPFPTKYIKRSGYQAIIPYVVALFSAGLLYYAAYLRKN 69
Db      11  AFAFGLGNVISMTFLAPLPFPTRYIKRSGTEGFSVPYVALFSAMLMIFYALKSN 70
Qy      70  YLVISNGFCALIELTYISLFLFYAPRKSRIPTGWM-LLELGCALGMVNPITYLAEGSH 128
Db      71  TPLITITNAGCVETIETIYIMVLYAPRKAKLFTAKIMALLNGVFGVILLITLLFRGSK 130
Qy      129  RVMIVGMICAINVAAPLPSIMROVITKRSVEFMPFTLSFLTCATWMPFYGFKKD 188
Db      131  RVALLGWICVGSFVSFVAPLSIMRVIOTKRSVEFMPFSLISLTJVSAVVMFLYGLIKD 190
Qy      189  FYIAFPNIIGFLFGLIYQMLLYFYKDSKRIDDEKSDPVEATKSKG-----VEIIT 240
Db      191  KYVALPNIIGFTGVQVGLYVLYNM-----KTPVAATLAEKADAGKLSSAADHVLV 242
Qy      241  NI 242
Db      243  NI 244
```

```

1      RESULT 5
2      US-10-425-114-59391
3      Sequence 59391, Application US/10425114
4      Publication NO. US20040034888A1
5      GENERAL INFORMATION:
6      APPLICANT: Liu, Jingdong
7      APPLICANT: Zhou, Yihua
8      APPLICANT: Kovalic, David K.
9      APPLICANT: Screen, Steven E
10     APPLICANT: Tabaska, Jack E
11     APPLICANT: Cao, Yongwei
12     TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
13     TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
14     FILE REFERENCE: 38-21(53313)B
15     CURRENT APPLICATION NUMBER: US/10/425,114
16     CURRENT FILING DATE: 2003-04-28
17     NUMBER OF SEQ ID NOS: 73128
18     SEQ ID NO 59391
19     LENGTH: 311
20     TYPE: PRT
21     ORGANISM: Zea mays
22     FEATURE:
23     OTHER INFORMATION: Clone ID: LIB3060-096-A1_F11.pep
24     US-10-425-114-59391

```

Query Match	48.3%	Score 653.5	DB 15	Length 311
Best Local Similarity	50.4%	Pred. No. 4e-54		
Matches	122	Conservative	49	Mismatches 54, Indels 17, Gaps 3
Qy	10	SPTGLGNIVSFMVFLAPVPTFFYKIYRKSGEGYQAIPYNAVLFAGLLLYAYLRNKA	69	
Db	20	AFAGGLGNIVSFMFLAPIPPTFFYKIYRKSGEGYQAVVAVLFSAMLMIFYALIKNE	79	
Qy	70	YLIVSINGFGCAIETLYSLFLFYAPRKSIFPTGLM-LLELVGAGMWDPIYLLAEGSH	128	
Db	80	TELLTINAGCVIETIYVMVFYVAPKAKLFTAKIMVLNNGVSGVILLTLTLFLPKSK	139	
Qy	129	RVMIVGIMCAAINAVFAPAPISINRQVITKYSVEEMPTLSLFTLCATMWFYGFPEKDD	188	
Db	140	RVYLLGWCVGFSVSFVAAPISIMRIVIQTYSVEVEMPTLSLSTLSAVMFLYGLTKD	199	
Qy	189	FYIAFPNITLFGIVQMLLFVYVDSKRIDDEKSDPREATKSKG-----VEIIT	240	
Db	200	KYVALPNITLFGIVQMVLVLYLNN-----KTPVAATMEGDAGKLSGADEHYLV	251	
Qy	241	NI 242		
Db	252	NI 253		

RESULT 6
 US-10-425-115-214286
 Sequence 214286, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants
 FILE REFERENCE: 38-21(53222) B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 214286
 LENGTH: 273
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_127027C.1.pep
 US-10-425-115-214286

	Query Match	48.3%	Score 653;	DB 17;	length 273;
	Best Local Similarity	51.0%;	Pred.	No. 3.8e-54;	
	Matches	123;	Conservative	47;	Mismatches 55; Indels 16; Gaps 3.
Oy	10 SPFI G LGNIVSFMVFLAPVPFTFYKIKRKSSGQALPYNVALFSAGLLYYAYLRKNA	69			
Dd	11.AFA G LGNIVSFMTPLAPIPTFPIRIKXSTBEFGSPYVVALLPSANLWLFYALKRNE	70			
Oy	70 YLI V SINGFCALIELTYISLEFPYAPRSKSIFTGMWL-LTELGLGMVMPITYLIAEGSH	128			
Dd	71 TFLITINAA G CVIETIIYVMFYVAPPKAKLFTAKIMALLINGGVGVIILLTLTLLFKGSK	130			
Oy	129 RVMIVGMTCAALINAVFAAPLPISIRKOVIKTYSVFEMPPITLSLFTLTCA T MMFFYGFPFKD	188			
Dd	131 RVVLIGMTCVGFSPSVFVAPLSIMRRVIQTGSVEYMPPSLSLTSLSAV M FVLGLLIKD	190			
Oy	189 FYIAFPNI L IGLFGIVOMLVFYVKDKSRIDEXSDPFRATRSKEG-----VEITIIN	241			
Dd	191 KYVALLPNVLGI F GVGVQNVLLVFEYMN-----KTPVAAAVGVGDAGKLPSAAD E HVALVN	242			
Oy	242 I 242				
Dd	243 I 243				

```

RESULT 7
US-10-425-114-47055
; Sequence 47055, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47055
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700332286_F1.1.pep
US-10-425-114-47055

```

Query Match	48.3%	Score 653	DB 15	Length 335
Best Local Similarity	51.0%	Pred. No. 4	9e-54	
Matches	123	Conservative	47	Mismatches 55; Indels 16; Gaps 3;
Oy	10	SPITGLGNIVSENVFLAPVPTFFYKIKYKSSSEGOAIPIYVALFSAGLLYAYALRKNA	69	
Db	45	AFAAGLLGNIVSEFMTFLAPVPTFFRIKYSKSTBGSOSIPYVALFASALMIFYALIKSNE	104	
Oy	70	YLIVSINGGCAIRLELYTISLFLFYAPAPRSKSTFTGMWL-TLELGLAGMWPIITYLLAEGSH	128	
Db	105	TEFLTINNAAGVIEITYIYVMFYVAPFKKALFTAKIALNLNGVPGVILLLTLTLFLFKSK	164	
Oy	129	RVMIVGMICAAINVAVPAAPLSIRKQVYKTKSVSEFMPTLSLFTLCATMFPFYGGFFKCD	188	
Db	165	RVLVLGMICVGFSSVFPVAPLSIRKRVYIQTGSVEYMPFSLSLSTLSAVMFLVGLLLYKD	224	
Oy	189	FYIAFPNIGLFGSIYOMLYFYVVKDSKRIDKSDPVRATKSKEG-----VEIIN	241	
Db	225	KYVALPVLGRIPEVGVOMLYVFTMN-----KTPVAAVAAGDAGCLPSAABEHVLVN	276	
Oy	242	I	242	
Db	277	I	277	

```

RESULT 8
US-10-425-115-214276
; Sequence 214276, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 214276
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127018C.1.pep
US-10-425-115-214276

```

Query Match	48.1%	Score 650.5	DB 17	Length 302
Best Local Similarity	50.0%	Pred. No. 7.4e-54		
Matches	121	Conservative	49	Mismatches 55; Indels 17; Gaps 3
QY	10	SPIRGLGNIVSFMWFLAPVPLPEFYKITYRKSSGQOALPIYVALFSAGLLLYYAVLRQNA	69	
DB	11	AFAGGLGNIVSFMFLAPIPLEFYAIYKSKSREGQSPYVALFSAMLMIFYAIKNE	70	
QY	70	YLIVSINGGCAIELTYSLFLEFYPRKSKIFTGLM-LLELGAIGMWPIYLLAEQSH	128	
DB	71	TELITINAGCVIEITLYVMFYVAPPKAKLETATIMALLNGVGVILLTLTLFKSKS	130	
QY	129	RVMIVGRTCAALINAVPAPISIMRQVITKITSVEBMPITLSIFLTLCATMFFYGFPEKDD	188	
DB	131	RVLVLGMCVGFSSVFAVAPISIMRIVIQIOTSVEBMPSTLSITLSVWVELYGLIKD	190	
QY	189	FYIAFPNIGFLFGVOMLLFVYVYDSKRIDEDKSDPREATKSKREG-----VEITII	240	
DB	191	KYVALPNTLGIIFGVYOMLVLYFYNN-----KTPAATAVNGDACKLPSADENHVLV	242	
QY	241	NI	242	
DB	243	NI	244	

```

RESULT 9
US-10-424-599-142919
Sequence 142919, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 142919
LENGTH: 254
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847.10006C.1.pep
US-10-424-599-142919

```

Query Match	48.0%;	Score 649.5;	DB 15;	Length 254;
Best Local Similarity	48.2%;	Pred. No. 7,5e-54;		
Matches	121;	Conservative	65;	Mismatches 60; Indels 5; Gaps 4;
QY	4	LRADDLSITFGLLGNIVSFMVFLAPVPFFYKTIYKRKSEGGQAIAPYMWALTSAGLLIYYA	63	
DB	3	MHRBSWAVFVGMNGIISFGVFLAPLPFFYQIYKKRSIEGQSILPYVALTSAMLIYYA	62	
QY	64	YL-RRNAALIVSINGFGCAIELTYSLEFLYAPRKSIFT-GMLMLELGAIGMWPIITY	121	
DB	63	FVKRKTALLITINMFGIVGESIYLSIFLIYAPKRPRITTKLLLLNVPFGAMLTSTL	122	
QY	122	LLABSRHWLVGMICAAINAVPAAPISIMROVYIKTSVSFMPPTLSLFTLCATMFF	181	
DB	123	YLSKAKKALAIIGWCIJENISVPAAPFIIRVYIKTSVSFMPPTLSMFTLINAVMFF	182	
QY	182	YGFKKDFYIAFPNIGLFGIVOMLIFYVYKSSRIDEKSDPVREATKSEGEVLI-I	240	
DB	183	YGLLRDYVALPMTLIGVFQIIGVMYIMWRNTPVLE--EPYKQELNGHIIDVKI	240	
QY	241	NIEDGNSDNL	251	
DB	241	GTMENHGAV	251	

```

RESULT 10
US-10-437-963-170840
/ Sequence 170840, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 170840
/ LENGTH: 319
/ TYPE: PRF
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(319)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_69127C.1.pep
US-10-437-963-170840

```

[illegible]

Db 192 VFVALLPNVLGFVFGVAQMALVMAVRSKKPLVASSSSAVVAA-----GLEI 236

RESULT 11
US-10-767-701-46186
; Sequence 46186, Application US/10767701
; Publication No. US20040172684A1

Query Match	47.9%	Score 647.5	DB 16	Length 304
Best Local Similarity	50.9%	Pred. No. 1.4e-53		
Matches 119, Conservative	49	Mismatches 65	Indels 1	Gaps 1

```
QY      189 FYIAFPNIGLFGIVOMLLFYVKDSKRIDKSDPVRATSKSGVEIINI 242
        |||||::|||::: : : : ::||
DB      191 KYALPNIGFTFVGVMVLYLVLTNNKTPVAVAEGKDAGGKLPSADEHVLVNI 244
```

Query Match	47.8%	Score 646.5	DB 16	Length 303
Best Local Similarity	49.8%	Pred. No. 1.8e-53		
Matches 119	Conservative 54	Mismatches 55	Indels 11	Gaps 2

```

      189 FYIAFPNITGLFGLVQMLLYFYVKDSKRIDDEKSDPHEATKTSLEGVEIINIIEDONS 217
      191 KYVAIPNVLGFSFGVIGMLYAMYNRS-----TPKAVLTKEVEAATATGDDHS 239

```

```

; FEATURE:
; OTHER INFORMATION: CLONE ID: TRIAE-23APR03-C866_1.F
US-10-739-930-10939

```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21002C.1.pep
US-10-437-963-117614

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2004, 20:31:31 ; Search time 55 Seconds
(without alignments)
319,532 Million cell updates/sec

Title: US-09-743-885a-1
Perfect score: 1353
Sequence: 1 MAQLRADDSFIFGLGNIV.....NSDNALQSMKXDPRLRTSK 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195.5	14.4	221	US-09-599-360B-104	Sequence 104, App
2	107.5	7.9	380	US-08-902-853-3	Sequence 3, Appl1
3	103.5	7.6	140	US-09-270-767-40416	Sequence 40416, A
4	103.5	7.6	140	US-09-270-767-55632	Sequence 55632, A
5	101	7.5	252	US-09-248-796A-26937	Sequence 26937, A
6	101	7.5	370	US-09-199-737-2	Sequence 2, Appl1
7	101	7.5	370	US-08-900-230-2	Sequence 2, Appl1
8	101	7.5	370	US-09-058-333A-2	Sequence 2, Appl1
9	100.5	7.4	462	US-09-328-352-5497	Sequence 5497, Ap
10	99	7.3	287	US-09-543-681A-5282	Sequence 5282, Ap
11	99	7.3	381	US-09-134-001C-3972	Sequence 3972, Ap
12	99	7.3	335	US-09-134-000C-3441	Sequence 5441, Ap
13	98.5	7.3	567	US-09-711-164-409	Sequence 409, App
14	98	7.2	294	US-09-328-352-7553	Sequence 7553, Ap
15	98	7.2	325	US-09-328-352-5760	Sequence 5760, Ap
16	97.5	7.2	482	US-09-328-352-7784	Sequence 7784, Ap
17	97	7.2	222	US-09-543-681A-4858	Sequence 4858, Ap
18	97	7.2	440	US-09-248-796A-20408	Sequence 20408, A
19	95	7.0	202	US-09-198-452A-1082	Sequence 1082, Ap
20	93.5	6.9	515	US-09-489-039A-8208	Sequence 8208, Ap
21	93.5	6.9	518	US-09-252-991A-31586	Sequence 31586, Ap
22	92.5	6.8	351	US-09-944-807-2	Sequence 2, Appl1
23	92.5	6.8	720	US-09-134-000C-5631	Sequence 5631, Ap
24	92	6.8	554	US-09-614-891-11	Sequence 11, Appl1
25	91.5	6.8	344	US-08-467-947A-8	Sequence 8, Appl1
26	91.5	6.8	344	US-08-467-947A-8	Sequence 8, Appl1
27	91.5	6.8	605	US-09-583-110-4773	Sequence 4773, Ap

28	90.5	6.7	439	US-09-583-110-4467	Sequence 4467, Ap
29	90.5	6.7	1226	US-08-540-804-12	Sequence 12, Appl
30	90.5	6.7	1226	US-08-218-265-12	Sequence 12, Appl
31	90.5	6.7	1226	US-08-521-877-12	Sequence 12, Appl
32	90.5	6.7	1226	US-08-590-399-12	Sequence 12, Appl
33	90.5	6.7	1226	US-08-916-247A-2	Sequence 2, Appl1
34	90	6.7	514	US-09-679-686B-22	Sequence 22, Appl1
35	89.5	6.6	308	US-09-328-352-7093	Sequence 7093, Ap
36	89.5	6.6	561	US-09-328-352-4759	Sequence 4759, Ap
37	89.5	6.6	597	US-09-328-352-4703	Sequence 4703, Ap
38	88.5	6.5	138	US-09-543-681A-6829	Sequence 6829, Ap
39	88.5	6.5	473	US-09-134-001C-3564	Sequence 3564, Ap
40	88.5	6.5	664	US-09-268-140-2	Sequence 2, Appl1
41	88	6.5	219	US-09-543-681A-5930	Sequence 5930, Ap
42	88	6.5	395	US-09-489-039A-9507	Sequence 9507, Ap
43	88	6.5	415	US-09-134-001C-5101	Sequence 5101, Ap
44	88	6.5	437	US-09-134-001C-4808	Sequence 4808, Ap
45	87.5	6.5	412	US-09-710-279-368	Sequence 368, Ap

ALIGNMENTS

RESULT 1
US-09-599-360B-104
Sequence 104, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bouguetieret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET 050C93
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 104
LENGTH: 221
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -28...-1
US-09-599-360B-104

Query Match 14.4%; Score 195.5; DB 4; Length 221;
Best Local Similarity 25.5%; Pred. No. 9.4e-13;
Matches 53; Conservative 48; Mismatches 94; Indels 13; Gaps 4;

QY	10	SRIFGLGNIVFMFLAVPTFFYKIKRKSSEGVQATYMAALSAGLLYYAVYRKNA	69
DB	9	SLIYGAC-VFTLGMFSAGLSLRHRMTRSDVNOQFLPTEVVNNGLSYGALKGGG	67
QY	70	YIVISNGFGCAIEILYISLPLFYAPRKSKIFTGMLMLELALGVMPITY----	124
DB	68	ILIV-VNTGALLOTLYILAYHYCRKR-----VLLQTKTLGCVLLGCGYFWLVP	120
QY	125	ESSHRMIVGWCIAINAVFAAPISIMKQIKTSVEFMPTLSLFTLCATMFFYGP	184
DB	121	NPEARLQGLGFCVSFTISMYSPLADLAKVIGTSTGCLSYPLTATLTLSASWCLYGF	180
QY	165	FKKDPYIAFPNLGLPGLGVOMLYFVY	212
DB	181	RURDPYIMVSNPGLVTSFIRFWLFWKY	208

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RESULT 2
US-08-902-853-3
; Sequence 3, Application US/08902853
; Patent No. 5945330
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Puri
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,853
; FILING DATE: Herewith
; CLASSIFICATION: ?
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0245 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HMT2NOT01
; CLONE: 493014
; US-08-902-853-3

Query Match 7.6%; Score 107.5; DB 2; Length 380;
Best Local Similarity 27.6%; Pred. No. 0.0044;
Matches 70; Conservative 28; Mismatches 109; Indels 47; Gaps 14;

QY 1 MAQLRADLSPFIRGLGNISFWFLAPVPFYIKRKSEGV---QATP-----YMW 52
DB 130 LKFKREASMRTEFLA-FLAGAAVVDKPFYDM--KRWEGYPIOSTIPSOYWMIE 186
QY 53 L-ESAGLLLYAYAKNAAYLVISINGCAIELTYISLFLFYAPRKSKIFGWMLELG 111
DB 187 LSFYWSLLFSIASDVKKDKPEQIHHVATITILSFWMFANY-----IRAG 232
QY 112 ALGWMV--PTTYLIAESGSHRMVIGWICAAINV-AVPAAPLSIMROYIKTKSVFMPFTL 168
DB 233 TLIMALHDSDDYL-ESAKMFNYAGMKNTCNNIFIVAFIITRLVI-----LPFWI 284
QY 169 SLFTLLCATMWFGEFKDQFYIAFPHILGL-----FGIVOMLLYVYKDSKIDEXS 223
DB 285 -LHCTLVYPELVPAFGYGFNSMVGVLQHLIFAMAYLIRMAKFI--TGKLVEDERS 341
QY 224 DPVEATKSKGV 237
DB 342 D--RETTESSEGE 353
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RESULT 3
US-09-270-767-40416
; Sequence 40416, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40416
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-40416

Query Match 7.6%; Score 103.5; DB 4; Length 140;
Best Local Similarity 27.7%; Pred. No. 0.003;
Matches 26; Conservative 19; Mismatches 40; Indels 9; Gaps 1;

QY 133 VGMICAINVAAPALSLIMROYIKTKSVFMPFTLSLFTLLCATMWFYGFKKDQFYIA 192
DB 45 LGMILGITLWVMVGSPLHLPKTIKSKSTEGMPFPIIFAGNLVAFSMTLYAISIKTVMV 104
QY 193 FPNILGFLFGIVOMLYFVY-----KDSKR 217
DB 105 LQNLILLVLGGIQLSMFAIYPNKPAAEKPKDSKK 138

RESULT 4
US-09-270-767-55632
; Sequence 55632, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55632
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-55632

Query Match 7.6%; Score 103.5; DB 4; Length 140;
Best Local Similarity 27.7%; Pred. No. 0.003;
Matches 26; Conservative 19; Mismatches 40; Indels 9; Gaps 1;

QY 133 VGMICAINVAAPALSLIMROYIKTKSVFMPFTLSLFTLLCATMWFYGFKKDQFYIA 192
DB 45 LGMILGITLWVMVGSPLHLPKTIKSKSTEGMPFPIIFAGNLVAFSMTLYAISIKTVMV 104
QY 193 FPNILGFLFGIVOMLYFVY-----KDSKR 217
DB 105 LQNLILLVLGGIQLSMFAIYPNKPAAEKPKDSKK 138

RESULT 5
US-09-248-796A-26937
; Sequence 26937, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/248, 796A
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;;
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 26937
LENGTH: 252
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-26937

Query Match 7.5%; Score 101; DB 4; Length 252;
Best Local Similarity 24.0%; Pred. No. 0.012;
Matches 56; Conservative 37; Mismatches 98; Indels 42; Gaps 10;

QY 43 GYQAIPIYVAL-ESAGL--LYYAYLRKNAVLIIVSINGFGCAIELTYISLFLYAPRKS 99
DB 17 GAQSVFCIVVLGASGFLADVGVNDRVTPALVSI-----LNLTYSYILLMPTILK 70
QY 100 IFTGMLLELALGAWMPITYLLAGSHRVMVGMCAINAVFAAPLSIMROYIKK 159
DB 71 NFSPSVIIL--VAEFIFVFYSAMGALAAVIPSQSG--DYGSYSSACSIKALI--- 122
QY 160 SVEFMFPTLSLFTLCATMWFYGF-----FKDFYIAFPNIGLFGIVQMLLY 209
DB 123 -----PFTLFNMLFATSEFLGIGYGFIPGVSSRGFSITLPA-----REFGAIPTDPA 172
QY 210 FVYKDSKRIDEXSD-PVREATKSKGVE---IINIEDNSDMLQSMED 257
DB 173 LFGKKYAVTDPVTDAIANAEVTSIGIENDAPKVASVGDNEATVGLASSEED 225

RESULT 6
US-09-199-737-2
Sequence 2, Application US/09199737A
Patent No. 6287788
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
APPLICANT: Borowsky, Beth
APPLICANT: Smith, Kelli E.
APPLICANT: Branchek, Theresa A.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
FILE REFERENCE: 52241-D-PC1-US
CURRENT APPLICATION NUMBER: US/09/199,737A
CURRENT FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Rat
US-09-199-737-2

Query Match 7.5%; Score 101; DB 3; Length 370;
Best Local Similarity 21.6%; Pred. No. 0.021;
Matches 46; Conservative 40; Mismatches 67; Indels 60; Gaps 10;

QY 9 LSFIFGLGNIVSFMVFLAPVPTFYKIYKRKSESG-----YQAIPIYVAL 53
DB 26 LIFLLGMVNGVLAVLLOPGPS---AWQEPSTTDLFIINLAVADLCFLICVPOQAI 82
QY 54 FSAGLLYYAYLRKNAVLIIVSINGFGCAIELTYISLFLYA-----PRSKIF 101
DB 83 YTLDAWLFQAFVCKTCHLITLTMVYASSFTLAIVSLDRYLAVRHPLRSRALRTPRARAA 142
QY 102 TG--WMLLELALGAWMPITY--LAEGRHVMIVGICA--AINAVFAA-----PLS 150
DB 143 VGLVWL-----LAALFSAPIYSYGTIVRYGALGELCVPMEDARRALDVATFAAGYLLPVA 198
QY 151 IMROYIKTSVEFMFPTLSLFTLCATMWFYGF 183

DB 199 VV-----SLAYGRTLCLFLWAAGV 216

RESULT 7
US-08-900-230-2
Sequence 2, Application US/08900230
Patent No. 6329197
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,230
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET INFORMATION: 52241-C/JPW/ADM
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NOS: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE:
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-900-230-2

Query Match 7.5%; Score 101; DB 3; Length 370;
Best Local Similarity 21.6%; Pred. No. 0.021;
Matches 46; Conservative 40; Mismatches 67; Indels 60; Gaps 10;

QY 9 LSFIFGLGNIVSFMVFLAPVPTFYKIYKRKSESG-----YQAIPIYVAL 53
DB 26 LIFLLGMVNGVLAVLLOPGPS---AWQEPSTTDLFIINLAVADLCFLICVPOQAI 82
QY 54 FSAGLLYYAYLRKNAVLIIVSINGFGCAIELTYISLFLYA-----PRSKIF 101
DB 83 YTLDAWLFQAFVCKTCHLITLTMVYASSFTLAIVSLDRYLAVRHPLRSRALRTPRARAA 142
QY 102 TG--WMLLELALGAWMPITY--LAEGRHVMIVGICA--AINAVFAA-----PLS 150
DB 143 VGLVWL-----LAALFSAPIYSYGTIVRYGALGELCVPMEDARRALDVATFAAGYLLPVA 198
QY 151 IMROYIKTSVEFMFPTLSLFTLCATMWFYGF 183
DB 199 VV-----SLAYGRTLCLFLWAAGV 216

RESULT 8
US-09-058-333A-2
Sequence 2, Application US/09058333A
Patent No. 6368812
GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A
APPLICANT: Borowsky, Beth
APPLICANT: Smith, Kelli E
TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/058,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEFAX: 212 391 0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-333A-2

Query Match
Best Local Similarity 7.5%; Score 101; DB 3; Length 370;
Matches 46; Conservative 40; Mismatches 67; Indels 60; Gaps 10;

QY 9 LSPFGLGNIVSFMVFLAPVPTFYKIKYKRSSEG-----YQALPYWAL 53
DB 26 LIFPLGAVNGVLAVLLOPEPS--AMQEPSTTDLPILNLAVALDCLFLCCVFPQAAI 82

QY 54 FSAGLIYYAVLRKNAVLIVSINGFGCAIETLYISLFLFYA-----PRKSKIF 101
DB 83 YTLDAWLFQGAFCVCTVHLLIYLTMYASSFTLAASLDRIYLAVRHPLASRALRTRNRRA 142

QY 102 TG--WMMLBGLGALGVMPITY--LLAEGSHRVMIVGICA--AINAVFPA-----PLS 150
DB 143 VGLVWL-----LAALFSAPLYSLSYGVTVRYGALCLCVPAWEDARRRDLVATFAAGYLLPVA 198

QY 151 IMROVITKSVEMFPFTLSLFLTCATMWFYGF 183
DB 199 VV-----SLAYGRTLC-FLMAAVG 216

RESULT 9
US-09-328-352-5497
Sequence 5497, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5497
LENGTH: 462
TYPE: PRT

ORGANISM: Acinetobacter baumannii
US-09-328-352-5497

Query Match
Best Local Similarity 7.4%; Score 100.5; DB 4; Length 462;
Matches 56; Conservative 42; Mismatches 92; Indels 57; Gaps 13;

QY 11 FIFGLGNIVSFMVFLAPVPTFYKIKYKRSSEGYQALPYWALP-----SA 56
DB 224 FFIGALLAIYVFRIRGLLET--QSPFKNAQAEFDQPKSGFALFKHPKAEFTVLELTAG 281

QY 57 GLLIYYAVLRKNAVLIVSINGFGC--AIELTYISLFLYAPRKSIFTLGL-----M 106
DB 282 GTLAFYTYTYYLOKYLVNMSGFTKRPBATOITTLALPFCLOP--LAGALSRIQGRKL 338

QY 107 LLELGLGWMVPITYLLAE--GSHRVMIVGIC-----AAINAVFAPAPLSIMR 153
DB 339 MIAFGYTGVL--FTYILFDLTANTHMYTAFWLCGLGLMVTGYTSINAVKA---ELFP 393

QY 154 QVITKSVEMFPFTLSLFLTCATMWFYGFYK--KQFYAFPNILGFLFGIYQMLY 209
DB 394 AHIRALGVA-LPYAIAINTL-FGDTAEFFALSPKAGHESWFIYVIMIF-----ISLLY 447

QY 210 FVYKDSK 216
DB 448 IFMKDKT 454

RESULT 10
US-09-543-681A-5282
Sequence 5282, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5282
LENGTH: 287
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5282

Query Match
Best Local Similarity 7.3%; Score 99; DB 4; Length 287;
Matches 47; Conservative 35; Mismatches 85; Indels 78; Gaps 7;

QY 18 NIVSFMVFLAPVPTFYKIKYKRSSEGYQALPYW--VALPSAGLLIYYAVLRKNAVLIVS 74
DB 28 SIYAVCAVLSLSTVFIPLPSLRKQNGYRGALLPAAVVALYTHAISLKFILFRPHSGONLS 87

QY 75 INFGCAIETLYISLFLYAPRKSIFGTWMLLELGLGWMVPITYLLAEGSHRVMIVG 134
DB 88 LTNLGAIVSLMVCVINTIVASR-----GRAMFLPIYCYCS-----IVN 126

QY 135 WTCADIN-----VAVFAAPLSIMROVITKSVEM 164
DB 127 LIIAALMPGFVTHLESSTSLPIHIGIALISYATLLIALLALYALQSLWLDYQLNKKTKES 186

QY 165 P-----FTLS-----LFLTCATMWFYGFYKDYIAFPNIGFLFGYQV 206
DB 187 PQMPPLMSIERKMFHTYGVVLLTLTCLGLLMDNIFGE-----NIHKSIFSIIAM 240

QY 207 LLYFV 211
DB 241 FVYII 245

RESULT 11
US-09-134-001C-3972
Sequence 3972, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3972
LENGTH: 381
TYPE: PR1
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3972

Query Match 7.3%; Score 99; DB 3; Length 381;
Best Local Similarity 20.3%; Pred. No. 0.035;
Matches 52; Conservative 40; Mismatches 80; Indels 84; Gaps 12;
15 LGNITSPM-----VFLAPVPTFYKIKRKSEGYQAIPTWALFSA-----56
168 ILSNVSYSITSTFSTFVLWVFFILYMKDEKFP--IPAIKFKGKERKVVVDLKD 225
57 -----GLLYVAVLRKNAVLIIVSINGGCAIELTYISLFLFYAPRK 97
226 LNTLSYIOGVTVSIIIGIILYIGY-----TIGLPTPLVLAVAGVA 270
98 SKI-FTG-WMLLELALGAV-MPTVYLLAEGSHRVAVICAMINAVFAAPL--SIW 152
271 NLIPFLGPWLSFAPAAIIGIIDGSTFI-----WVCV---VTLIAQQLGNAV 315
153 ROVIKRSVEFMPTLSLFTLCATMFFPGFKPKDYIAFPNIGLFGIYVQMLLYFY 212
316 TPNVWKSLSIHPLTIIIVLAAIGLGF-----TILVAVP-----LVAVIKTLVSNIF 365
213 KDSKRIIDKSDPVRE 228
366 KYRQRIYDKANSVND 381

RESULT 12
US-09-134-000C-5441
Sequence 5441, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5441
LENGTH: 395
TYPE: PR1
ORGANISM: Enterococcus faecalis
US-09-134-000C-5441

Query Match 7.3%; Score 99; DB 4; Length 395;
Best Local Similarity 23.7%; Pred. No. 0.037;
Matches 49; Conservative 35; Mismatches 93; Indels 30; Gaps 8;
18 NIVFVFLAPVPTFYKIKRKSEGYQAIPTW-----VALFSAGLLLYVLRKNAVLIIV 73

DB 3 SVVKTLLGLGFIPSW-----RKKKEHDLPMWFGWTFMPS-YVLYEIIIRGTAFFLI 56
74 SINGRCALIELTYISLFLFYAPRKSKIFTGMLLELALGAMWPTIT-----YLLAG 126
57 PLAPFG-----LFLAFYFKERKRLNGTLFVLVLTATYIGTARITNNVFLITL 107
127 SRWMIWGMICAMINAVFAAPLSIMROYIKTSVEFMPTLSLFTLCATMFFYGFPK 186
108 AIIAIIATITALLAKRLYALITFLYNNAVVWKRKSRSLNLTLLATIGTLIIYNF- 166
187 KDFYIAFPNIGLFGIYVQML-YPVY 212
167 --FQSLPTWLSLPLTIAFPILTYFAF 191

RESULT 13
US-09-711-164-409
Sequence 409, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 409
LENGTH: 567
TYPE: PR1
ORGANISM: Escherichia coli
US-09-711-164-409

Query Match 7.3%; Score 98.5; DB 4; Length 567;
Best Local Similarity 20.2%; Pred. No. 0.068;
Matches 56; Conservative 48; Mismatches 86; Indels 87; Gaps 14;
23 MYFLAPVPTFYKIKRKSEGYQAIPTWALF---SAGLLY---AYLRKNAVLIIVSIN 76
1 MAVSERELIVKIPSKIDFTLAPFYSISIFPLCSGLPFGYFPAFTKGCY-----54
77 GFGCAIELTYISLFLFYAPRKSKIFTGMLLELALGAMWPTIYLLAEGSHRV-----130
55 --ECSWKLDYIKQFYF-----SLETAWYL--ISAVAFIASVFI---QRIKAYLT 99
131 MYVWICAAI-----NVAFAAPLSIMROYIKTSVEFMPTLSLFTLCATMFF 180
100 LAITWIVLTITDVALIHADNIAMNNIILNIIYNL-----FGAILSLFNCLSNLI 152
181 FVGFPKDYIAFPNIGLFGIYVQML-----LYEVYKDSKRIIDKSDPVREATK 231
153 HANKIKH-----IPILSMIPVLSAIIIAIITAYIILF-----188
232 SKGEVLIINIEDNSDNA---LQSEKDFSLRTSK 265
189 AROAVEIEMDI-SEGSDIAYGVKDNESFGFLNDK 224

RESULT 14
US-09-328-352-7553
Sequence 7553, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2004, 18:58:30 ; Search time 118 Seconds
(without alignments)
805.621 Million cell updates/sec

Title: US-09-743-885A-1
Perfect score: 1353
Sequence: 1 MAQRADRLSIFLGLGNIV.....NSDNLQSMEXDFSLRTSK 265

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980a:*
- 2: geneseqp1990a:*
- 3: geneseqp2000a:*
- 4: geneseqp2001a:*
- 5: geneseqp2002a:*
- 6: geneseqp2003a:*
- 7: geneseqp2003b:*
- 8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1353	100.0	265	3	AAVS8647
2	1353	100.0	265	3	AAV44803
3	704.5	52.1	258	3	AA643420
4	703.5	52.0	258	3	AA624273
5	623.5	46.1	292	3	AA606230
6	622	46.0	289	3	AA654308
7	622	46.0	289	3	AA626337
8	622	46.0	289	8	ADN73901
9	621.5	45.9	289	3	AA649770
10	621.5	45.9	289	3	AA621971
11	618	45.7	285	3	AA641683
12	615.5	45.5	289	7	ABM73930
13	615	45.5	289	7	ABM73783
14	590	43.6	294	3	AA642299
15	564.5	41.7	281	3	AA642959
16	564.5	41.7	304	3	AA607674
17	488.5	36.1	195	3	AA63421
18	488.5	36.1	195	3	AA642274
19	447	33.0	247	8	ADM7668
20	447	33.0	247	8	ADM47960
21	433.5	32.0	234	3	AA649771
22	433.5	32.0	234	3	AA621972
23	431.5	31.9	231	3	AA621973
24	431.5	31.9	231	3	AA649772
25	431	31.9	228	3	AA641684

26	429	31.7	291	8	ADM47961	Adm47961 Polypepti
27	427.5	31.6	235	3	AA606231	Aag06231 Arabidops
28	411	30.4	239	3	AA642300	Aag42300 Arabidops
29	403.5	29.8	251	3	AA651964	Aag51964 Arabidops
30	401.5	29.7	232	3	AA642301	Aag42301 Arabidops
31	400.5	29.6	251	3	AA619711	Aag19711 Arabidops
32	399.5	29.5	226	3	AA642960	Aag42960 Arabidops
33	399.5	29.5	249	3	AA607675	Aag07675 Arabidops
34	395	29.2	300	7	ABM74461	Abm74461 DNA clone
35	383.5	28.3	258	3	AA616725	AA616725 Arabidops
36	363.5	26.9	239	3	AA646827	AA646827 Arabidops
37	363.5	26.9	239	3	AA611624	AA611624 Arabidops
38	353.5	26.1	225	3	AA622336	AA622336 Arabidops
39	353.5	26.1	236	3	AA622335	AA622335 Arabidops
40	350	25.9	202	3	AA617669	AA617669 Arabidops
41	337	24.9	200	3	AA654309	AA654309 Arabidops
42	337	24.9	200	3	AA626338	AA626338 Arabidops
43	328.5	24.3	203	3	AA606232	Aag06232 Arabidops
44	323.5	23.9	185	3	AA641685	Aag41685 Arabidops
45	318.5	23.5	242	7	ABM73820	Abm73820 DNA clone

ALIGNMENTS

RESULT 1
AAVS8647
ID AAVS8647 standard; protein; 265 AA.

AC AAVS8647;
XX
DT 12-SEP-2003 (revised)
DT 11-APR-2000 (first entry)

DE Petunia nectary-specific NECT1 protein.

XX NECT1; nectary; nectar; transgenic plant; honey.

OS Petunia x hybrida.

XX EP974667-A1.

XX 26-JAN-2000.

PD 16-JUL-1998; 98EP-00202375.

PF 16-JUL-1998; 98EP-00202375.

PR 16-JUL-1998; 98EP-00202375.

XX (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.

XX Creemers J, Angenent GC, Kater MM;

XX WPI; 2000-108400/10.

XX N-PSDB; AA235493.

PT Novel DNA sequences used to produce modified honey, the metabolites of which can be isolated and purified.

PS Claim 1; Page 15; 56pp; English.

The present sequence is that of Petunia hybrida NECT1 protein that is highly expressed in the nectaries of petunia and weakly expressed in the stamens. The sequence was deduced from cDNA (see AA235493) obtained by differential display. The present invention provides a method for producing recombinant proteins in honey. The honey is manufactured by insects, preferably honeybees, that collect the nectar of transgenic plants. The NECT1 gene and its promoter (see AA235496) can be utilised in expression cassettes for the production of transgenic plants that produce a protein of interest in their nectar. The function of NECT1 has not yet been determined. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 265 AA;

5

Query Match 100.0%; Score 1353; DB 3; Length 265;
Best Local Similarity 100.0%; Pred. No. 9, 9e-151;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLRADDSIFIFGLGNIVSFVWFLAPVPTFYKIYKRKSSSEGYQAIPIYVVALFSAGLL 60
DB 1 MAQLRADDSIFIFGLGNIVSFVWFLAPVPTFYKIYKRKSSSEGYQAIPIYVVALFSAGLL 60

QY 61 YYAYLKRNAYLIYSINGFGCAIELTYISLFLYAPRKSIFFTGMLMLEGALGMVPIIT 120
DB 61 YYAYLKRNAYLIYSINGFGCAIELTYISLFLYAPRKSIFFTGMLMLEGALGMVPIIT 120

QY 121 YLLAEGSHRVMIVGICAAINVAFAAPLSIMRQVITKTSVEFMPFTLSFLTLCATMWF 180
DB 121 YLLAEGSHRVMIVGICAAINVAFAAPLSIMRQVITKTSVEFMPFTLSFLTLCATMWF 180

QY 181 FYGPFKKDFIAPFNITIGFLGIQVQLLYFYVYKDSKRIDEKSDPVREATKSKRGVEIIT 240
DB 181 FYGPFKKDFIAPFNITIGFLGIQVQLLYFYVYKDSKRIDEKSDPVREATKSKRGVEIIT 240

QY 241 NIEDDNSDNALQSMEXKDFSLRLRTSK 265
DB 241 NIEDDNSDNALQSMEXKDFSLRLRTSK 265

RESULT 2
AAV44803
ID AAV44803 standard; protein; 265 AA.
XX
AC AAV44803;
XX
DT 12-SEP-2003 (revised)
DT 17-MAY-2000 (first entry)
XX
DE Petunia hybrida nectary-specific protein NECL.
XX
KM NECL; nectary-specific protein; metabolite; recombinant protein;
KM transgenic plant; nectar; honey; insect; bee; pharmaceutical; enzyme;
KM biotect; antioxidant; food additive.
XX
OS Petunia x hybrida.
XX
PN WO200004176-A1.
XX
PD 27-JAN-2000.
XX
PF 15-JUL-1999; 99WO-NL000453.
XX
PR 16-JUL-1998; 98EP-00202375.
PR 14-DEC-1998; 98EP-00204215.
XX
PA (CPRO-) CPRO-DILO CENIT PLANTENVERDELINGS REPROD.
XX
PI Creemers J, Angenent GC, Kater MM;
XX
DR WPI, 2000-182438/16.
DR N-PSDB; AAZ50200.
XX
PT New DNA encoding Petunia hybrida nectary-specific proteins, useful for,
XX e.g. producing modified honey.
XX
PS Claim 1; Page 39; 93pp; English.
XX
CC The present sequence is a nectary-specific protein NECL which was
CC isolated from nectaries of Petunia hybrida strain W15 using mRNA
CC differential display system. NECL resembles membrane protein and is
CC strongly expressed in the nectaries of P. hybrida. A DNA sequence from
CC the promoter region upstream of nectary-specific expressed sequence e.g.
CC NECL and FBPI5 DNAs is used in a recombinant DNA construct comprising a
CC DNA encoding a metabolite preferably recombinant protein, a DNA encoding
CC a signal peptide that targets the recombinant protein to the nectar and
CC optionally a signal sequence functional in plants for the transcription
CC termination and polyadenylation of an RNA molecule. The DNA construct is

CC useful for producing transgenic plants which excrete recombinant proteins
CC in its nectar. The nectar is processed into honey by insects (preferably
CC bees) and the desired protein is easily recovered from it. The
CC recombinant proteins are useful for pharmaceutical purposes, as enzymes
CC for biotect and antioxidants for food additives. (Updated on 12-SEP-2003
CC to standardise OS field)

SQ Sequence 265 AA;

Query Match 100.0%; Score 1353; DB 3; Length 265;
Best Local Similarity 100.0%; Pred. No. 9, 9e-151;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLRADDSIFIFGLGNIVSFVWFLAPVPTFYKIYKRKSSSEGYQAIPIYVVALFSAGLL 60
DB 1 MAQLRADDSIFIFGLGNIVSFVWFLAPVPTFYKIYKRKSSSEGYQAIPIYVVALFSAGLL 60

QY 61 YYAYLKRNAYLIYSINGFGCAIELTYISLFLYAPRKSIFFTGMLMLEGALGMVPIIT 120
DB 61 YYAYLKRNAYLIYSINGFGCAIELTYISLFLYAPRKSIFFTGMLMLEGALGMVPIIT 120

QY 121 YLLAEGSHRVMIVGICAAINVAFAAPLSIMRQVITKTSVEFMPFTLSFLTLCATMWF 180
DB 121 YLLAEGSHRVMIVGICAAINVAFAAPLSIMRQVITKTSVEFMPFTLSFLTLCATMWF 180

QY 181 FYGPFKKDFIAPFNITIGFLGIQVQLLYFYVYKDSKRIDEKSDPVREATKSKRGVEIIT 240
DB 181 FYGPFKKDFIAPFNITIGFLGIQVQLLYFYVYKDSKRIDEKSDPVREATKSKRGVEIIT 240

QY 241 NIEDDNSDNALQSMEXKDFSLRLRTSK 265
DB 241 NIEDDNSDNALQSMEXKDFSLRLRTSK 265

RESULT 3
AAG43420
ID AAG43420 standard; protein; 258 AA.
XX
AC AAG43420;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54268.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN BP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.

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PR	23-JUL-1999	99US-01451455
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PR	26-JUL-1999	99US-01452766
PR	27-JUL-1999	99US-01455137
PR	27-JUL-1999	99US-01459199
PR	28-JUL-1999	99US-01459512
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PR	02-AUG-1999	99US-01463987
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PR	01-SEP-1999	99US-01519307
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PR	04-OCT-1999	99US-01571177
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PR	13-OCT-1999	99US-01592957
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PR	18-OCT-1999	99US-01595847
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PR	21-OCT-1999	99US-01607677

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PR 21-OCT-1999;	99US-0160814P.			
PR 21-OCT-1999;	99US-0160815P.			
PR 22-OCT-1999;	99US-0160980P.			
PR 22-OCT-1999;	99US-0160981P.			
PR 22-OCT-1999;	99US-0160989P.			
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PR 26-OCT-1999;	99US-0161359P.			
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Query Match	52.1%;	Score 704.5;	DB 3;	Length 258;
Best Local Similarity	55.1%;	Pred. No. 3.7e-74;		
Matches 136;	Conservative 48;	Mismatches 62;	Indels 1;	Gaps 1
Db	4	LRADLSTFGLTGNIVSFVFLAPVPFYYKYKKRSEGVQAIPIYVALFAGLLVYA	63	
Db	3	LKHRIALFLGLTGNIVSFVFLSVVPFYYKYKKRSEGVQAIPIYVALFAGLLVYA	62	
Qy	64	YLKRNAYLIVSINGFCALIEYLYISLFLFYAPRKSKIFTGWMLD-ELGALGMVPIYL	122	
Db	63	IMKTHAYLISINTGCFLEISYFLYLILYAPREAKISTKLKIVACNIGGLLLLVNL	122	
Qy	123	LAEGSHRPMYIGMCAINNVAPAPLSIMROYITKSYEENPFLSLFLITCATMWPY	182	
Db	123	LVPKQHRSTYVGWCACAAVSLAVFASPLSVMRKVITKSYEENPFLSLFLITNAVMWPY	182	
Qy	183	GFFKDFPIYAPNIIIGFLFGIVQMLTYVYKDSKRIDDEKSDPVEATKSKGEIINI	242	
Db	183	GLIKDKKTIAMPNIIGFLFGVAGMILYMYQGSTKTDLPTENQLANKTDVNEVPIVAVEL	242	
Qy	243	EDDNSDN	249	
Db	243	PDVGSND	249	
RESULT 4				
AAAG24273				
ID	AAAG24273	standard; protein; 258 AA.		
XX	AAAG24273;			
AC				
XX				
DT	17-OCT-2000	(first entry)		
XX				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 27884.			
XX				
KW	Protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KW	termination sequence.			
XX				
OS	Arabidopsis thaliana.			
XX				
PN	EP1033405-A2.			
XX				
PD	06-SEP-2000.			
XX				
PF	25-FEB-2000; 2000EP-00301439.			
XX				
PR	25-FEB-1999; 99US-0121825P.			
PR	05-MAR-1999; 99US-0123180P.			
PR	09-MAR-1999; 99US-0123548P.			
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PR	29-MAR-1999; 99US-0126785P.			
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PR	06-APR-1999; 99US-0128234P.			

PR	16-APR-1999;	99US-01286741
PR	16-APR-1999;	99US-01286454
PR	16-APR-1999;	99US-01300777
PR	21-APR-1999;	99US-01305449
PR	23-APR-1999;	99US-01305100
PR	23-APR-1999;	99US-01308911
PR	28-APR-1999;	99US-01314441
PR	30-APR-1999;	99US-01320048
PR	30-APR-1999;	99US-01324077
PR	04-MAY-1999;	99US-01324644
PR	05-MAY-1999;	99US-01324659
PR	06-MAY-1999;	99US-01324877
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PR	18-JUN-1999;	99US-01397631
PR	21-JUN-1999;	99US-01398171
PR	22-JUN-1999;	99US-01398991
PR	23-JUN-1999;	99US-01400531
PR	23-JUN-1999;	99US-01403541
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QY 64 YLRKNAVLYVLSINGFCALIELTYISLFLFYAPRKSKIFTGWLMLL-ELGALGMVPTLYL 122
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D 123 LVPKQHRVSTGVCAAYSLAVFASPLSVMRKVIKTSVEYMPFLSLSTLINAVMPPFY 182
QY 183 GFPKKDFYIAPNIIIGFLPGIVQMLFYFYKDSKRIDDEKSDPVREATKSGEVEIINI 242
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 2928.
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridization assay; genetic mapping; gene expression control; promoter;
termination sequence.
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OS Arabidopsis thaliana.
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PF 25-FEB-2000; 2000EP-00301439.
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XX AAG54308;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 69231.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
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XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 30756.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
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RESULT 9
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
XM termination sequence.
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RESULT 12
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AC
XX

ABM73930;

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DE
XX

XX
OS
XX

Hordeum vulgare.

XX
PD
XX

17-JUL-2003.

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PR	20-DEC-2001; 2001JP-00403300
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XX	
PI	Sato K, Takeda K, Kohara Y,
XX	

PT Single nucleotide polymorphism sites in barley varieties and DNA PT sequences containing them for analysis and identification of barley PT varieties and production of barley transformants with desired

[illegible]

DR	WPI: 2003-587127/55.
XX	Single nucleotide polymorphism sites in barley varieties and DNA
PT	sequences containing them for analysis and identification of barley
PT	varieties and production of barley transformants with desired
PT	characteristics.
PS	Disclosure; SEQ ID XX; 284bp; Japanese.
XX	
CC	The present invention relates to oligonucleotide clones originating in
CC	barley (<i>Hordeum vulgare</i>) which contain single nucleotide polymorphisms
CC	(SNP). The oligonucleotides may be used for analysis of SNPs among barley
CC	varieties; identification of particular varieties and genotype-phenotype
CC	analyses; isolation of specific genes and creation of new varieties by
CC	transformation of barley varieties with them and production of new barley
CC	varieties with desired properties. The present sequence represents an
CC	oligonucleotide clone sequence featured in the specification. The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published-pct-sequences
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SQ	Sequence 268 AA;
Query Match	45.5%; Score 615; DB 7; Length 268;
Best Local Similarity	49.6%; Pred. No. 1.5e-63;
Matches 121; Conservative	45; Mismatches 56; Indels 20; Gaps 4
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OY	129 RVMIVGMCAINNAVFAAPISIKROVKTKTSVERMPETLSLFLTLCAFMFFVGFPPKDD 188
Db	131 RVVSLGMCVGFSPVCFAPAPLSITIGRAVTKTSVEVMPSPSLTTLTSLAVWMLYGLLKD 190
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PR	25-OCT-1999	99US-016100599
PR	25-OCT-1999	99US-016140409
PR	25-OCT-1999	99US-016140549
PR	25-OCT-1999	99US-016140669
PR	26-OCT-1999	99US-016135359
PR	26-OCT-1999	99US-016136060
PR	26-OCT-1999	99US-016136161
PR	28-OCT-1999	99US-016192309
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PR	29-OCT-1999	99US-016214220

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Best Local Similarity	50.8%;	Pred. NO. 1.4e-57;		
Matches 121;	Conservative 39;	Mismatches 65;	Indels 13;	Gaps 5;

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Search completed: December 24, 2004, 20:40:42
Job time : 121 secs

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PR	22-JUL-1999	99US-01451922P
PR	23-JUL-1999	99US-01451455P
PR	23-JUL-1999	99US-01452185P
PR	23-JUL-1999	99US-01452244P
PR	26-JUL-1999	99US-01452766P
PR	26-JUL-1999	99US-01459133P
PR	27-JUL-1999	99US-01459189P
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